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OM protein - protein search, using bw model

Run on: September 15, 2005, 13:56:25 ; Search time 170 Seconds
(without alignments)
1012.402 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256

Sequence: 1 AGABEVVLPPIKISGVNLT.....GCTRKTPPPDVLSTFVN 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq19808:*
2: geneseq19908:*
3: geneseq20008:*
4: geneseq20018:*
5: geneseq20028:*
6: geneseq20038:*
7: geneseq20038:*
8: geneseq20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	445	AAE09792	Aae09792 Eleusine
2	2199.5	97.5	444	AAW27301	Aaw27301 Maize 5-e
3	2199.5	97.5	444	AAW28461	Aaw28461 Maize 5-e
4	2199.5	97.5	444	AAW44824	Aaw44824 Mutant ma
5	2199.5	97.5	444	AAW4871	Aab67871 5-enolpyr
6	2199.5	97.5	444	ADRE7918	Adre7918 Wild type
7	2199.5	97.5	444	ADRE7921	Adre7921 Wild type
8	2198.5	97.5	444	AAW27302	Aaw27302 Maize 5-e
9	2198.5	97.5	444	AAW28462	Aaw28462 Maize 5-e
10	2198.5	97.5	444	AAW44825	Aaw44825 Mutant ma
11	2198.5	97.4	570	ADJ79601	Adj79601 Corn BPSP
12	2196.5	97.0	444	AAW70529	Aaw70529 Mutant ma
13	2187.5	96.0	444	AAW28463	Aaw28463 Maize 5-e
14	2165.5	96.0	511	AAW23065	Aaw23065 Modified
15	2165	96.0	511	ADQ37121	Adq37121 Cell prot
16	2165	96.0	511	ADQ15707	Adq15707 Rice stire
17	2164	95.9	515	ADJ79594	Adj79594 Rice EPSP
18	2130.5	94.4	442	AAW27802	Aaw27802 BPSP synt
19	1927	85.4	448	ADRE7919	Adre7919 Wild type
20	1927	85.4	516	AAW65136	Aaw65136 A. Petunia
21	1927	85.4	516	AAW67870	Aab67870 5-enolpyr
22	1920	85.1	516	AAW32774	Aaw32774 Petunia B
23	1911	84.7	516	AAW65137	Aaw65137 Brasica
24	1911	84.7	516	AAW67869	Aab67869 5-enolpyr
25	1905	84.4	444	AAW23061	Aaw23061 Modified

26	1902	84.3	451	8	ADRE7920	Adre7920 Wild type
27	1901	84.3	452	3	AAW36512	Aaw36512 Arabidops
28	1901	84.3	465	3	AAW40465	Aaw40465 Arabidops
29	1901	84.3	520	3	AAW40464	Aaw40464 Arabidops
30	1901	84.3	520	5	ABW92125	Abw92125 Herbicida
31	1901	84.3	578	3	AAW40463	Aaw40463 Arabidops
32	1899.5	84.2	521	6	AAW27798	Aaw27798 BPSP synt
33	1897	84.1	521	6	ABR39998	AbR39998 A. thalia
34	1894	84.0	525	8	ADJ79598	Adj79598 Soybean E
35	1893	83.9	464	3	AAW34722	Aaw34722 Arabidops
36	1893	83.9	521	3	AAW34721	Aaw34721 Arabidops
37	1888	83.7	520	4	AAW67847	Aab67847 5-enolpyr
38	1885.5	83.6	445	2	AAW27800	Aaw27800 BPSP synt
39	1879	83.3	444	2	AAW23063	Aaw23063 Modified
40	1871.5	83.0	444	2	AAW23064	Aaw23064 Modified
41	1867	82.8	444	2	AAW23062	Aaw23062 Modified
42	1863.5	82.6	440	2	AAW27799	Aaw27799 BPSP synt
43	1843.5	81.7	496	2	AAW27801	Aaw27801 BPSP synt
44	1682	74.6	391	3	AAW36513	Aaw36513 Arabidops
45	1674	74.2	391	3	AAW34723	Aaw34723 Arabidops

ALIGNMENTS

RESULT 1	
ID	AAE09792 standard; protein; 445 AA.
XX	
XX	AAE09792;
XX	
DT	29-NOV-2001 (first entry)
XX	
DE	Eleusine indica BPSP synthase mature protein.
XX	
KM	Goose grass; glyphosate herbicide; N-phosphonomethylglycine; BPSPs;
KW	5-enolpyruvylshikimate-3-phosphate synthase; phosphoenolpyruvate; PEP;
KM	transgenic plant.
XX	
OS	Eleusine indica.
XX	
PN	WO200166704-A2.
XX	
PD	13-SEP-2001.
XX	
PF	06-MAR-2001; 2001WO-US007135.
XX	
PR	09-MAR-2000; 2000US-0188093P.
XX	
PA	(MONS) MONSANTO TECHNOLOGY LLC.
XX	
PI	Baerson SR, Heck GJ, Rodriguez DJ;
XX	
DR	WPI; 2001-557661/62.
XX	
PT	N-PSDB; AAD16837.
XX	
PT	Novel DNA molecule encoding naturally occurring glyphosate resistant 5-
XX	enolpyruvylshikimate-3-phosphate synthase enzyme derived from glyphosate
XX	tolerant plant species useful for producing glyphosate tolerant plants.
PS	Claim 5; Fig 2; 69pp; English.
XX	
CC	The patent discloses methods and compositions for making plants tolerant
CC	to glyphosphate (N-phosphonomethylglycine) herbicide. The invention
CC	relates to novel glyphosate resistant 5-enolpyruvylshikimate-3-phosphate
CC	synthase (BPSPs) enzyme from Eleusine indica (goose grass), where the
CC	enzyme has a K.m for phosphoenolpyruvate (PEP) of less than 10 M. BPSPs
CC	genes are useful for producing glyphosate tolerant transgenic plants by
CC	inserting BPSPs gene into the genome of a plant cell, obtaining a
CC	transformed plant cell, and regenerating from the transformed plant cell
CC	a genetically transformed plant which has increased tolerance to
CC	glyphosate herbicide. The present sequence is BPSP synthase mature
CC	protein from Eleusine indica

XX Sequence 445 AA;

Query Match 100.0%; Score 2256; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 2.3e-193;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAEEVVLQPIKEISGVVVKLPGSKSLNSRILLLSALAEGLTVVDNLNSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKEISGVVVKLPGSKSLNSRILLLSALAEGLTVVDNLNSEDVHYMLGALK 60
QY 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNAGTAMRSLTAAVTAAGNAT 120
DB 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNAGTAMRSLTAAVTAAGNAT 120
QY 121 YVLDGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 180
DB 121 YVLDGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 180
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGQ 240
DB 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGQ 240
QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTW 300
DB 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTW 300
QY 301 TETSVTVTGPPREPFGKRLKALIDVNNMKMPDVAMTLAVVALPADGPTAIRDVASRWYKE 360
DB 301 TETSVTVTGPPREPFGKRLKALIDVNNMKMPDVAMTLAVVALPADGPTAIRDVASRWYKE 360
QY 361 TERMVAIIRTELTKLGSVVEGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 420
DB 361 TERMVAIIRTELTKLGSVVEGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 420
QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
DB 421 TIRDPGCTRKTPPDYFDVLSTFVK 445

RESULT 2
AAW27301
ID AAW27301 standard; protein; 444 AA.
XX
AC AAW27301;
XX
DT 17-OCT-2003 (revised)
DT 17-NOV-1997 (first entry)
XX
DE Maize 5-enolpyruvylshikimate-3-phosphate synthase.
XX
KM plant expression regulation sequence; intron; histone; BPSPS;
KM 5-enolpyruvylshikimate-3-phosphate synthase; wild-type; corn;
KM herbicide tolerance; glyphosate; PRPA-WL-715; PRPA-WL-716.
OS Zea mays; (strain Black Mexican Sweet).
XX
PN WO9704114-A2.
XX
PD 06-FEB-1997.
XX
PF 17-JUL-1996; 96MO-FR001109.
XX
PR 19-JUL-1995; 95FR-00008980.
XX
PA (RHON ) RHONE POULENC AGROCHIMIE.
XX
PI Deroose R, Chaubet N, Gigot C;
XX
DR WPI; 1997-132652/12.
XX
DR N-PSDB; AAT85994.
XX
PT New regulatory sequence for chimeric gene expression in rapidly growing

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PT parts of a plant - includes at least one intron from a plant histone gene
PT and is useful for imparting resistance to herbicides.

PS Example 1; Page 22; 31pp; French.

XX A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
CC (BPSPS) gene) was amplified from total DNA of Arabidopsis thaliana (var.
CC columbia) using PCR primers having the sequences given in AAT85991 and
CC AAT85992. Using the amplified fragment as a probe, the wild-type BPSPS
CC gene was isolated from a maize BMS cDNA library. The BPSPS gene can be
CC mutated to increase a plant's tolerance to certain herbicides, including
CC glyphosate. The mutated gene is incorporated into an expression vector
CC containing a plant promoter and an intron sequence derived from the 5'-
CC non-coding region of a plant histone gene. The intron enhances expression
CC of the herbicide tolerance gene in rapidly growing parts of plants. The
CC intron can also be used to enhance expression of genes that impart
CC resistance to pathogens or that encode nutritional or therapeutic
CC proteins. The present sequence represents the wild-type maize BPSPS
CC enzyme. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 2; Length 444;
Best Local Similarity 97.5%; Pred. No. 2.7e-188;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```

QY 1 AGAEEVVLQPIKEISGVVVKLPGSKSLNSRILLLSALAEGLTVVDNLNSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKEISGVVVKLPGSKSLNSRILLLSALAEGLTVVDNLNSEDVHYMLGALK 60
QY 61 TLGLSVLEADKAKRAVAVVGGCGKFPVEKDAAKEEVQLFLGNAGTAMRSLTAAVTAAGNAT 120
DB 61 TLGLSVLEADKAKRAVAVVGGCGKFPVE-DAKEEVQLFLGNAGTAMRPLTAAVTAAGNAT 119
QY 121 YVLDGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 180
DB 120 YVLDGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKYKLSGSIS 179
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGQ 240
DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSMRPFYIKGQ 239
QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTW 300
DB 240 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLOGDVKFAEVLMMGAKVTW 299
QY 301 TETSVTVTGPPREPFGKRLKALIDVNNMKMPDVAMTLAVVALPADGPTAIRDVASRWYKE 360
DB 300 TETSVTVTGPPREPFGKRLKALIDVNNMKMPDVAMTLAVVALPADGPTAIRDVASRWYKE 359
QY 361 TERMVAIIRTELTKLGSVVEGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 420
DB 360 TERMVAIIRTELTKLGSVVEGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 419
QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
DB 420 TIRDPGCTRKTPPDYFDVLSTFVK 444

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RESULT 3
AAW28461
ID AAW28461 standard; protein; 444 AA.
XX
AC AAW28461;
XX
DT 17-OCT-2003 (revised)
DT 17-NOV-1997 (first entry)
XX
DE Maize 5-enolpyruvylshikimate-3-phosphate synthase.
XX
KM 5-enolpyruvylshikimate-3-phosphate synthase; BPSPS; wild-type; corn;
KM herbicide tolerance; glyphosate; PRPA-WL-716.
XX
XX

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OS Zea mays; (strain Black Mexican Sweet).
 XX
 PN MO9704103-A2.
 XX
 PD 06-FEB-1997.
 XX
 PF 18-JUL-1996; 96MO-FR001125.
 XX
 PR 19-JUL-1995; 95FR-00008979.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 XX
 PI Lebrun M., Salland A., Freyesinet G,
 XX
 DR WPI, 1997-132642/12.
 XX
 DR N-PSDB; AAT86001.
 XX
 PT New mutant gene for 5-enol pyruvylshikimate-3-phosphate synthase -
 PT encodes an enzyme in which ile replaces thr at position 102 to give
 PT increased tolerance for glyphosate and related herbicides.

Example 1; Page 19-20; 26pp; French.

XX A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
 CC (EPSPS) gene was amplified from total DNA of Arabidopsis thaliana (var.
 CC Columbia) using PCR primers having the sequences given in AAT85998 and
 CC AAT85999. Using the amplified fragment as a probe, the wild-type EPSPS
 CC gene was isolated from a maize (strain Black Mexican Sweet) cDNA library.
 CC The EPSPS gene can be mutated to increase a plant's tolerance to certain
 CC herbicides, including glyphosate. The present sequence represents the
 CC wild-type maize EPSPS enzyme. Claimed mutant genes encode EPSPS in which
 CC at least wild-type Thr at position 102 has been replaced by Ile.
 CC Additional mutations are of Pro at position 106 to Ser and Gly at
 CC position 101 to Ala. (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 2; Length 444;

Best Local Similarity 97.5%; Pred. No. 2.7e-188;
 Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```

QY 1 AGAEEVLOPIKEISGVVGLPGSKLSNRILLLSALAEETTVDNLNSEDVHYMLGALK 60
DB 1 AGAEEVLOPIKEISGVVGLPGSKLSNRILLLSALAEETTVDNLNSEDVHYMLGALK 60
QY 61 TTGLSVADKAKRAVAVVGGCGKFPVEKDAKEEVQFLGNAGTAMRSLTAATAAGNAT 120
DB 61 TTGLSVADKAKRAVAVVGGCGKFPVE-DAKEEVQFLGNAGTAMRSLTAATAAGNAT 119
QY 121 VYLDGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKVLSGSIS 180
DB 121 VYLDGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKVLSGSIS 179
QY 120 VYLDGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKVLSGSIS 179
DB 120 VYLDGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKVLSGSIS 179
QY 181 QYLSALLMAAPLALGVVEIIEIDKLISIPVENTLILMERFGKASHSDMFYIKGQ 240
DB 181 QYLSALLMAAPLALGVVEIIEIDKLISIPVENTLILMERFGKASHSDMFYIKGQ 239
QY 180 QYLSALLMAAPLALGVVEIIEIDKLISIPVENTLILMERFGKASHSDMFYIKGQ 239
DB 180 QYLSALLMAAPLALGVVEIIEIDKLISIPVENTLILMERFGKASHSDMFYIKGQ 239
QY 241 KYKSPKNAVVEGDASSAYFLAGAAITGGTVVEGGGTSLSQDVKFAVLEMMGAKVTM 300
DB 240 KYKSPKNAVVEGDASSAYFLAGAAITGGTVVEGGGTSLSQDVKFAVLEMMGAKVTM 299
QY 301 TETSIVTGPORPPRRKRLKALDVNMNKKPDMVAMTLAVVALPADPTAIRDVAASRVKE 360
DB 300 TETSIVTGPORPPRRKRLKALDVNMNKKPDMVAMTLAVVALPADPTAIRDVAASRVKE 359
QY 361 TERHVAIRTELTDGASVEBGLDYCIITPEPKLNTAIDTYDHRMAAFSLAACADVRY 420
DB 360 TERHVAIRTELTDGASVEBGLDYCIITPEPKLNTAIDTYDHRMAAFSLAACADVRY 419
QY 421 TTRDPCCTRTKTPDYFDVLSFVKN 445
DB 420 TTRDPCCTRTKTPDYFDVLSFVKN 444

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RESULT 4

AAW44824
 ID AAW44824 standard; protein; 444 AA.

XX
 AC AAW44824;
 XX

DT 23-NOV-1998 (first entry)

XX Mutant maize EPSPS encoded by clone pRPA-MU-716.

XX Transgenic plant; resistance: herbicide; chimaeric gene; tolerance; PCR;
 KW hydroxyphenylpyruvate dioxygenase; isoxaflutole; sulcotriione; primer;
 KW amplification; tobacco; cotton; rape; soy; sugar beet; cereal; ioxynil;
 KW nitrilase; dihalohydroxybenzonitrile; bromoxynil; nematode; insecticide;
 KW glyphosate oxidoreductase; Bacillus thuringiensis; fungus; maize; EPSPS;
 XX 5-enolpyruvyl-3-phosphoshikimate synthase.

XX Zea mays.

OS
 XX
 PN MO9802562-A2.

PD 22-JAN-1998.

PF 10-JUL-1997; 97MO-FR001256.

PR 16-JUL-1996; 96FR-00009137.

PA (RHON) RHONE-POULENC AGROCHIMIE.

PI Pallett K., Deroose R., Pellissier B., Salland A;

DR WPI, 1998-110608/10.

DR N-PSDB; AAV19278.

XX Chimaeric gene imparting resistance to two or more herbicides - such as
 PT hydroxyphenylpyruvate dioxygenase inhibitors, also related vectors and
 PT transformed plants.

PS Example 2; Page 31-32; 49pp; French.

XX The invention relates to the generation of transgenic plants resistant to
 CC preferably at least 2 herbicides by introducing a chimaeric gene
 CC comprising at least 2 gene subunits where one sequence encodes
 CC hydroxyphenylpyruvate dioxygenase (HPPD), an enzyme that promotes
 CC tolerance to herbicides such as isoxaflutole or sulcotriione (see
 CC AAV19269). The plants, e.g. tobacco, cotton, rape, soy, sugar beet,
 CC cereals, may also contain a gene encoding e.g. a nitrilase for resistance
 CC to dihalohydroxybenzonitriles such as bromoxynil or ioxynil, glyphosate
 CC oxidoreductase for resistance to glyphosate. This sequence represents the
 CC maize 5-enolpyruvyl-3-phosphoshikimate synthase (EPSPS). The coding
 CC sequence contains a mutation in which the NcoI site at position 1217 is
 CC destroyed by site directed mutagenesis, which is a silent mutation and
 CC does not affect the sequence of the encoded protein. A third gene
 CC encoding a Bacillus thuringiensis insecticidal protein or proteins
 CC imparting resistance to fungi or nematodes, may also be introduced into
 CC the plant

XX Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 2; Length 444;

Best Local Similarity 97.5%; Pred. No. 2.7e-188;
 Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```

QY 1 AGAEEVLOPIKEISGVVGLPGSKLSNRILLLSALAEETTVDNLNSEDVHYMLGALK 60
DB 1 AGAEEVLOPIKEISGVVGLPGSKLSNRILLLSALAEETTVDNLNSEDVHYMLGALK 60
QY 61 TTGLSVADKAKRAVAVVGGCGKFPVEKDAKEEVQFLGNAGTAMRSLTAATAAGNAT 120
DB 61 TTGLSVADKAKRAVAVVGGCGKFPVE-DAKEEVQFLGNAGTAMRSLTAATAAGNAT 119
QY 121 VYLDGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKVLSGSIS 180
DB 121 VYLDGVPRRRERPIGDLVVGKQLGADVDCFLGTDCPPRVKIGLPGSKVLSGSIS 180

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|||||
Db      120 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSIS 179
Qy      181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Db      180 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 239
Qy      241 KYKSPKNAYVEGDASASAYFLAGAAITGCTVTEGGCTTSLQGDVKAFAVLEMMGAKVTM 300
Db      240 KYKSPKNAYVEGDASASAYFLAGAAITGCTVTEGGCTTSLQGDVKAFAVLEMMGAKVTM 299
Qy      301 TETSVTYTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVALLADGPTAIRDVASRWYK 360
Db      300 TETSVTYTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVALLADGPTAIRDVASRWYK 359
Qy      361 TERMAVAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMAFSLAACADV 420
Db      360 TERMAVAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMAFSLAACADV 419
Qy      421 TIRDPGCTRKTPFDYFDVLTSTFVN 445
Db      420 TIRDPGCTRKTPFDYFDVLTSTFVN 444

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RESULT 5
AAB67871 standard; protein; 444 AA.

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XX AC      AAB67871:
XX DT      29-JUN-2001 (first entry)
XX DE      5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) polypeptide.
XX OS      Zea mays.
XX PN      MO200124615-A1.
XX PD      12-APR-2001.
XX PF      10-OCT-2000; 2000MO-US027941.
XX PR      07-OCT-1999; 99US-0158027P.
XX RA      30-DEC-1999; 99US-0173564P.
XX PA      (VALT-) VALIGEN US INC.
XX PI      Beetham PR, Avlasar PL, Walker KA, Metz RA;
XX DR      WPI; 2001-273533/28.
XX PT      Novel non-transgenic herbicide resistant plant expressing mutant 5-
XX PT      enolpyruvylshikimate-3-phosphate synthase and the enzyme, plant retain
XX PT      catalytic activity and growth of wild-type gene product.
XX PS      Disclosure; Fig 4; 5pp; English.

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The present sequence represents a 5-enolpyruvylshikimate-3-phosphate synthase (EPSP synthase or EPSPs). The specification describes a non-transgenic herbicide resistant plant which expresses a mutant EPSPs gene product which has substantially the same level of catalytic activity as compared to the wild-type gene product, and which plant has substantially normal growth as compared to a plant expressing the wild-type EPSPs gene product. The mutated EPSPs protein allows for increased resistance or tolerance of a plant to the herbicide of the phosphonemethyl glycine family and allows for substantially normal growth or development of the plant, its organs, tissues or cells as compared to the wild-type plant irrespective of the presence or absence of the herbicide. The EPSPs is used in the production of non-transgenic herbicide (glyphosate) resistant plants such as corn, wheat, rice, barley, soybean, cotton, sugarbeet.

CC oilseed rape, canola, flax, sunflower, potato, tobacco, tomato, alfalfa, CC poplar, pine, eucalyptus, apple, lettuce, peas, lentils, grape, turf CC grass or Brascia sp

XX SQ Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 4; Length 444;
Best Local Similarity 97.5%; Pred. No. 2.7e-188;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```

Qy      1 AGAEEVLTQPIKEIGGVKLPSSKSLSNRIILLSLABETTYVDNLNSDVHYMLGALK 60
Db      1 AGAEEIVLQPIKEIGGVKLPSSKSLSNRIILLSABETTYVDNLNSDVHYMLGALKR 60
Qy      61 TLGLSEADKAKRNVVGGCGKFPVEKDAKEEVOLPIGNAGTAMRSILTAATTAAGNAT 120
Db      61 TLGLSEADKAKRNVVGGCGKFPVE-DAKEEVOLFENAGTAMRPLTAATTAAGNAT 119
Qy      121 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSIS 180
Db      120 YVLGVPKRRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSIS 179
Qy      181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Db      180 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 239
Qy      241 KYKSPKNAYVEGDASASAYFLAGAAITGCTVTEGGCTTSLQGDVKAFAVLEMMGAKVTM 300
Db      240 KYKSPKNAYVEGDASASAYFLAGAAITGCTVTEGGCTTSLQGDVKAFAVLEMMGAKVTM 299
Qy      301 TETSVTYTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVALLADGPTAIRDVASRWYK 360
Db      300 TETSVTYTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVALLADGPTAIRDVASRWYK 359
Qy      361 TERMAVAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMAFSLAACADV 420
Db      360 TERMAVAIRTELTKLGASVEEGDYCIITPEKLVNTAIDTYDDHRMAMAFSLAACADV 419
Qy      421 TIRDPGCTRKTPFDYFDVLTSTFVN 445
Db      420 TIRDPGCTRKTPFDYFDVLTSTFVN 444

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RESULT 6
ADR67918
ID ADR67918 standard; protein; 444 AA.
XX ADR67918;
XX AC ADR67918;
XX DT 18-NOV-2004 (first entry)
XX DE Wild type EPSPs from maize.
XX OS Zea mays.
XX PN WO2004074443-A2.
XX PD 02-SEP-2004.
XX PF 17-FEB-2004; 2004MO-US004636.
XX PR 18-FEB-2003; 2003US-0448438P.
XX PA (MONS) MONSANTO TECHNOLOGY LLC.
XX PI Alibhai MF, Cajacob C, Feng PCC, Heck GR, Qi Y, Flaasink S;
XX PI Stallings WC;

glyophosate resistant; class I;
KW 5-enolpyruvylshikimate-3-phosphate synthase; EPSPs; T1021; P106A; T1PA;
KW mutation; glyphosate tolerant plant; glyphosate; weed control; herbicide;
KW transgenic; plant.

DR WPI; 2004-635563/61.
 DR N-PSDB; ADR67921.
 XX
 PT New isolated DNA molecule that encodes a glyphosate resistant class I 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) protein, useful for
 PT preparing glyphosate tolerant plants.
 XX
 PS Example 1; Fig 1; 73pp; English.
 XX
 CC This sequence is encoded by an isolated DNA molecule that encodes a
 CC glyphosate resistant class I 5-enolpyruvylshikimate-3-phosphate synthase
 CC (EPSPS) protein. A variant of this sequence may be used in the method of
 CC the invention for preparing a glyphosate tolerant plant. The method
 CC comprises contacting a recipient plant cell with a DNA construct
 CC comprising the EPSPS sequence under the control of a plant specific
 CC promoter, that is incorporated into the genome of the recipient plant
 CC cell; regenerating the recipient plant cell into a plant; and applying an
 CC effective dose of glyphosate to the plant, where the plant displays a
 CC glyphosate tolerant phenotype. The resulting plants may be used in a
 CC method of controlling weeds in a field of glyphosate tolerant crop plants
 CC by applying to the field of glyphosate tolerant crop plant an effective
 CC dose of a glyphosate containing herbicide.
 CC
 SQ Sequence 444 AA;

Query Match 97.5%; Score 2199.5; DB 8; Length 444;
 Best Local Similarity 97.5%; Pred. No. 2.7e-188;
 Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVLPKSKLSNRILLLSALAEQTVVNDNLNSDVHYMLGALK 60
 DB 1 AGAEEVILQPIKEISGVVLPKSKLSNRILLLSALAEQTVVNDNLNSDVHYMLGALK 60
 QY 61 TLGLSVADYAKAAKRAVAVGCGGKFPVEKDAKEVQLFLNAGTAMRSLTAATTAAGNAT 120
 DB 61 TLGLSVADYAKAAKRAVAVGCGGKFPVE-DAKEVQLFLNAGTAMRPLTAATTAAGNAT 119
 QY 121 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVKVGIGLPGKVKYLSGSISS 180
 DB 120 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVVNGIGLPGKVKYLSGSISS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAESHSDMDFYIKGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAESHSDMDFYIKGQ 239
 QY 241 KYKSPKNAAYVEGDASASFFLAGAATGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 300
 DB 240 KYKSPKNAAYVEGDASASFFLAGAATGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 299
 QY 301 TETSVTVTGPORPFPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
 DB 300 TETSVTVTGPORPFPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRDVASWRVKE 359
 QY 361 TERHVAIRTELTKLGSVVEGLDYCIITPEKLNVTAIIDTYDDHRMAAFSLAACADVPY 420
 DB 360 TERHVAIRTELTKLGSVVEGLDYCIITPEKLNVTAIIDTYDDHRMAAFSLAACAEVY 419
 QY 421 TIRDPGCTKRTFPDYFDVLSFVYN 445
 DB 420 TIRDPGCTKRTFPDYFDVLSFVYN 444

RESULT 7
 ADR67921
 ID ADR67921 standard; protein; 444 AA.
 XX
 AC ADR67921;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Wild type EPSPS from maize.
 XX
 KW glyphosate resistant; class I;

KW 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; T1021; P106A; T1PA;
 KW mutation; glyphosate tolerant plant; glyphosate; weed control; herbicide;
 KW transgenic; plant.
 XX
 OS Patunia sp.
 XX
 PN WO2004074443-A2.
 XX
 PD 02-SBP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004636.
 XX
 PR 18-FEB-2003; 2003US-0448438P.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Alibhai MF, CaJacob C, Feng PCC, Heck GR, Qi Y, Piasinski S;
 PI Stallings WC;
 XX
 DR WPI; 2004-635563/61.
 XX
 PT New isolated DNA molecule that encodes a glyphosate resistant class I 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) protein, useful for
 PT preparing glyphosate tolerant plants.
 XX
 PS Example 1; Fig 2; 73pp; English.

This sequence represents an isolated class I 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) protein. This sequence is included in the scope of the invention for comparison with the variant EPSPS from maize. Variant EPSPS coding sequences may be used in the method of the invention for preparing a glyphosate tolerant plant. The method comprises contacting a recipient plant cell with a DNA construct comprising the EPSPS sequence under the control of a plant specific promoter, that is incorporated into the genome of the recipient plant cell; regenerating the recipient plant cell into a plant; and applying a glyphosate tolerant phenotype. The resulting plants may be used in a method of controlling weeds in a field of glyphosate tolerant crop plants by applying to the field of glyphosate tolerant crop plant an effective dose of a glyphosate containing herbicide.

Query Match 97.5%; Score 2199.5; DB 8; Length 444;
 Best Local Similarity 97.5%; Pred. No. 2.7e-188;
 Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVLPKSKLSNRILLLSALAEQTVVNDNLNSDVHYMLGALK 60
 DB 1 AGAEEVILQPIKEISGVVLPKSKLSNRILLLSALAEQTVVNDNLNSDVHYMLGALK 60
 QY 61 TLGLSVADYAKAAKRAVAVGCGGKFPVEKDAKEVQLFLNAGTAMRSLTAATTAAGNAT 120
 DB 61 TLGLSVADYAKAAKRAVAVGCGGKFPVE-DAKEVQLFLNAGTAMRPLTAATTAAGNAT 119
 QY 121 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVKVGIGLPGKVKYLSGSISS 180
 DB 120 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGDCPPRVVNGIGLPGKVKYLSGSISS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAESHSDMDFYIKGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAESHSDMDFYIKGQ 239
 QY 241 KYKSPKNAAYVEGDASASFFLAGAATGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 300
 DB 240 KYKSPKNAAYVEGDASASFFLAGAATGCTVVEGCGTISLQGDVKAFAVLEMMGAKVTW 299
 QY 301 TETSVTVTGPORPFPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
 DB 300 TETSVTVTGPORPFPGRKHLKAI DVNMNMKPDVAMTLAVVALPADGPTAIRDVASWRVKE 359
 QY 361 TERHVAIRTELTKLGSVVEGLDYCIITPEKLNVTAIIDTYDDHRMAAFSLAACADVPY 420

Db 360 TERWVAIRTELTKGASVEEGPDYCIITPEKLNVTALDITDDHRMAMAFSLAACAEVY 419
 QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445
 Db 420 TIRDPGCTRKTPPDYFDVLSTFVK 444

RESULT 8

AAW27302 standard; protein; 444 AA.

AAW27302;

17-NOV-1997 (first entry)

Maize 5-enolpyruvylshikimate-3-phosphate synthase double mutant.

XX plant expression regulation sequence; intron; histone; EPSPS;

KM 5-enolpyruvylshikimate-3-phosphate synthase; wild-type; corn;

XX herbicide tolerance; glyphosate; pRPA-ML-720.

OS Zea mays; (strain Black Mexican Sweet).

OS Synthetic.

Key Location/Qualifiers

FT M1sc-difference 102 /note= "Wild-type Thr has been replaced by Ile"

FT M1sc-difference 106 /note= "Wild-type Pro has been replaced by Ser"

PN WO9704114-A2.

PD 06-FEB-1997.

PF 17-JUL-1996; 96WO-FR001109.

XX 19-JUL-1995; 95FR-00008980.

XX (RHON) RHONE POULENC AGROCHIMIE.

PA Derose R, Chaubet N, Gligot C;

PI MPI; 1997-132652/12.

DR N-PSDB; AAT85995.

XX New regulatory sequence for chimeric gene expression in rapidly growing

PT parts of a plant - includes at least one intron from a plant histone gene

PT and is useful for imparting resistance to herbicides.

XX Example 1; Page 25; 31pp; French.

XX A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase

CC (EPSPS) gene) was amplified from total DNA of Arabidopsis thaliana (var.

CC Columbia) using PCR primers having the sequences given in AAT85991 and

CC AAT85992. Using the amplified fragment as a probe, the wild-type EPSPS

CC gene was isolated from a maize BMS CDNA library. The EPSPS gene can be

CC mutated to increase a plant's tolerance to certain herbicides, including

CC glyphosate. The present sequence represents a specific example of a EPSPS

CC double mutant in which the wild-type amino acids at positions 102 and 106

CC of the enzyme have been changed by site-directed mutagenesis of the EPSPS

CC gene. The mutated gene is incorporated into an expression vector

CC containing a plant promoter and an intron sequence derived from the 5'-

CC non-coding region of a plant histone gene. The intron enhances expression

CC of the herbicide tolerance gene in rapidly growing parts of plants. The

CC intron can also be used to enhance expression of genes that impart

CC resistance to pathogens or that encode nutritional or therapeutic

CC proteins

XX Sequence 444 AA;

SO Query Match 97.5%; Score 2198.5; DB 2; Length 444;

Best Local Similarity 97.5%; Pred. No. 3,4e-188;

Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVOPIKEISGVYKLGSSKSLSNRIILLSAAGTAVYNDNLNSEDVHYMGALK 60

Db 1 AGAEEVVOPIKEISGVYKLGSSKSLSNRIILLSAAGTAVYNDNLNSEDVHYMGALK 60

QY 61 TLGLSVEADKAKRAVWVGCGGKPFVEKDAKEVOLFLGNAGTAMRSILTAATAAGNAT 120

Db 61 TLGLSVEADKAKRAVWVGCGGKPFVE-DAKEVOLFLGNAGTAMRSILTAATAAGNAT 119

QY 121 YTLDGVPKRRERPIGDLVYGLKQLGADVDCFLGTCCPPYRVKIGLPGGKYKLSGSISS 180

Db 120 YTLDGVPKRRERPIGDLVYGLKQLGADVDCFLGTCCPPYRVKIGLPGGKYKLSGSISS 179

QY 181 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRIMERPGVKAHSDSMRFTYKGGQ 240

Db 180 QYLSALLMAAPLALGDVEIEIIDKLSIPYEMTLRIMERPGVKAHSDSMRFTYKGGQ 239

QY 241 KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTTSLOGDYKFAVLEMGAKYTW 300

Db 240 KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTTSLOGDYKFAVLEMGAKYTW 299

QY 301 TETSVTVTGPPREPGRKHLKAI DVNMNMKMPDVAMTLAVALLFADGPTAIRDVASWRVKE 360

Db 300 TETSVTVTGPPREPGRKHLKAI DVNMNMKMPDVAMTLAVALLFADGPTAIRDVASWRVKE 359

QY 361 TERWVAIRTELTKGASVEEGDYLITPEKLNVTALDITDDHRMAMAFSLAACADVPY 420

Db 360 TERWVAIRTELTKGASVEEGDYLITPEKLNVTALDITDDHRMAMAFSLAACAEVY 419

QY 421 TIRDPGCTRKTPPDYFDVLSTFVK 445

Db 420 TIRDPGCTRKTPPDYFDVLSTFVK 444

RESULT 9

AAW28462

ID AAW28462 standard; protein; 444 AA.

XX AAW28462;

XX 17-NOV-1997 (first entry)

XX Maize 5-enolpyruvylshikimate-3-phosphate synthase T1021, P106S mutant.

XX 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; wild-type; corn;

XX herbicide tolerance; glyphosate; pRPA-ML-720.

XX Zea mays; (strain Black Mexican Sweet).

OS Synthetic.

Key Location/Qualifiers

FT M1sc-difference 102 /note= "Wild-type Thr has been replaced by Ile"

FT M1sc-difference 106 /note= "Wild-type Pro has been replaced by Ser"

PN WO9704103-A2.

PD 06-FEB-1997.

PF 18-JUL-1996; 96WO-FR001125.

XX 19-JUL-1995; 95FR-00008979.

XX (RHON) RHONE POULENC AGROCHIMIE.

PA Lebrun M, Sailland A, Freysinet G;

PI MPI; 1997-132642/12.

DR N-PSDB; AAT86002.

PT New mutant gene for 5-enol pyruvylshikimate-3-phosphate synthase -

PT encodes an enzyme in which the replaces Thr at position 102 to give
 increased tolerance for glyphosate and related herbicides.

PS Claim 9, Page 22-23, 26pp; French.

XX A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
 (EPSPS) gene) using PCR primers having the sequences given in AAT85998 and
 CC Columbia) using PCR primers having the sequences given in AAT85998 and
 CC AAT85999. Using the amplified fragment as a probe, the wild-type EPSPS
 CC gene was isolated from a maize EMS CDNA library. The EPSPS gene can be
 CC mutated to increase a plant's tolerance to certain herbicides, including
 CC glyphosate. The present sequence represents a specifically claimed
 CC example of a EPSPS double mutant in which the wild-type amino acids at
 CC positions 102 and 106 of the enzyme have been changed by site-directed
 CC mutagenesis of the coding sequence (see features table)

XX Sequence 444 AA;

Query Match 97.5%; Score 2198.5; DB 2; Length 444;

Best Local Similarity 97.5%; Pred. No. 3.4e-188; Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVNDNLNSDEVHYMLGALK 60
 DB 1 AGAEEVILQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVNDNLNSDEVHYMLGALK 60
 QY 61 TLGLSVBADKAAKRAVAVVCGGKFPVEKDAKEVQFLGNAGTAMSLTAATTAAGGNAT 120
 DB 61 TLGLSVBADKAAKRAVAVVCGGKFPVE-DAKEEVQFLGNAGTAMSLTAATTAAGGNAT 119
 QY 121 YVLDGVPRMRERPIGDLVVGKLGADVDCFLGDCPPRVVKGIGLPGSKVLSGSIS 180
 DB 120 YVLDGVPRMRERPIGDLVVGKLGADVDCFLGDCPPRVVKGIGLPGSKVLSGSIS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVENTLRMERFGVKAHSDSWDRFYIKGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYVENTLRMERFGVKAHSDSWDRFYIKGQ 239
 QY 241 KYKSPKNAVVEGDASASYFLAGAAITGGTATVVEGCGTSSLOGDVKFAVLEMMGAKVTM 300
 DB 240 KYKSPKNAVVEGDASASYFLAGAAITGGTATVVEGCGTSSLOGDVKFAVLEMMGAKVTM 299
 QY 301 TETSVAVTGPORBPFGKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVVASRVKE 360
 DB 300 TETSVAVTGPORBPFGKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVVASRVKE 359
 QY 361 TERMAVIRTELTLTGASVEEGLDYCIITPPEKLNVTADITYDDHRMAMAFSLAACADVPV 420
 DB 360 TERMAVIRTELTLTGASVEEGLDYCIITPPEKLNVTADITYDDHRMAMAFSLAACADVPV 419
 QY 421 TIRDPGCTRTKTPFDYFVLTSTPVKN 445
 DB 420 TIRDPGCTRTKTPFDYFVLTSTPVKN 444

RESULT 10

AAW44825 AAW44825 standard; protein; 444 AA.

AC AAW44825;

DT 23-NOV-1998 (first entry)

XX Mutant maize EPSPS encoded by clone pRPA-ML-720.

XX Transgenic plant; resistance; herbicide; chimeric gene; tolerance; PCR;
 KM hydroxyphenylpyruvate dioxygenase; isoxaflutole; sulcotriole; primer;
 KM amplification; tobacco; cotton; rape; soy; sugar beet; cereals; ioxynil;
 KM nitrilase; dihalohydroxybenzoxitrile; bromoxynil; nematode; insecticide;
 KM glyphosate oxidoreductase; Bacillus thuringiensis; fungus; maize; EPSPS;
 KM 5-enolpyruvyl-3-phosphoshikimate synthase.
 XX Zea mays.

OS Synthetic.

PN MO9802562-A2.

PD 22-JAN-1998.

PP 10-JUL-1997; 97MO-FR001256.

PR 16-JUL-1996; 96FR-00009137.

XX (RHON) RHONE-BOULENC AGROCHIMIE.

PA Pallett K, Derose R, Pellesier B, Salland A;

DR WPI, 1998-110608/10.

DR N-PSDB; AAV19279.

PT Chimeric gene imparting resistance to two or more herbicides - such as
 hydroxyphenylpyruvate dioxygenase inhibitors, also related vectors and
 transformed plants.

PS Example 2, Page 35-36; 49pp; French.

XX The invention relates to the generation of transgenic plants resistant to
 CC preferably at least 2 herbicides by introducing a chimeric gene
 CC comprises at least 2 gene subunits where one sequence encodes
 CC hydroxyphenylpyruvate dioxygenase (HPPD), an enzyme that promotes
 CC tolerance to herbicides such as isoxaflutole or sulcotriole (see
 CC AAV19269). The plants, e.g. tobacco, cotton, rape, soy, sugar beet,
 CC cereals, may also contain a gene encoding e.g. a nitrilase for resistance
 CC to dihalohydroxybenzoxitriles such as bromoxynil or ioxynil, glyphosate
 CC oxidoreductase for resistance to glyphosate. This sequence represents a
 CC mutant maize 5-enolpyruvyl-3-phosphoshikimate synthase (EPSPS). The
 CC coding sequence contain mutations changing the amino acids G101A, T102I
 CC and P106S, which were generated by site directed mutagenesis. A third
 CC gene encoding a Bacillus thuringiensis insecticidal protein or proteins
 CC imparting resistance to fungi or nematodes, may also be introduced into
 CC the plant

XX Sequence 444 AA;

Query Match 97.5%; Score 2198.5; DB 2; Length 444;

Best Local Similarity 97.5%; Pred. No. 3.4e-188; Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVNDNLNSDEVHYMLGALK 60
 DB 1 AGAEEVILQPIKEISGVVKKLPGSKSLSNRIILLSALAEGLTVVNDNLNSDEVHYMLGALK 60
 QY 61 TLGLSVBADKAAKRAVAVVCGGKFPVEKDAKEVQFLGNAGTAMSLTAATTAAGGNAT 120
 DB 61 TLGLSVBADKAAKRAVAVVCGGKFPVE-DAKEEVQFLGNAGTAMSLTAATTAAGGNAT 119
 QY 121 YVLDGVPRMRERPIGDLVVGKLGADVDCFLGDCPPRVVKGIGLPGSKVLSGSIS 180
 DB 120 YVLDGVPRMRERPIGDLVVGKLGADVDCFLGDCPPRVVKGIGLPGSKVLSGSIS 179
 QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVENTLRMERFGVKAHSDSWDRFYIKGQ 240
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYVENTLRMERFGVKAHSDSWDRFYIKGQ 239
 QY 241 KYKSPKNAVVEGDASASYFLAGAAITGGTATVVEGCGTSSLOGDVKFAVLEMMGAKVTM 300
 DB 240 KYKSPKNAVVEGDASASYFLAGAAITGGTATVVEGCGTSSLOGDVKFAVLEMMGAKVTM 299
 QY 301 TETSVAVTGPORBPFGKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVVASRVKE 360
 DB 300 TETSVAVTGPORBPFGKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVVASRVKE 359
 QY 361 TERMAVIRTELTLTGASVEEGLDYCIITPPEKLNVTADITYDDHRMAMAFSLAACADVPV 420
 DB 360 TERMAVIRTELTLTGASVEEGLDYCIITPPEKLNVTADITYDDHRMAMAFSLAACADVPV 419

XX Sequence 570 AA; 97.4%; Score 2196.5; DB 2; Length 570;
 Query Match Best Local Similarity 97.3%; Pred. No. 7.3e-188;
 Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVVKLPGSKLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 60
 |||
 DB 127 AGAEEVVLQPIKISGVVVKLPGSKLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 186
 |||

QY 61 TLGLSTEADKAAKRAVAVVCGGKFPVEKDAKEEVOLFLGNAGTAMRSLTAAVTAAGNAT 120
 |||
 DB 187 TLGLSTEADKAAKRAVAVVCGGKFPVE-DAKEEVOLFLGNAGTAMRSLTAAVTAAGNAT 245
 |||

QY 121 YVLGVPRMRERPIGDLVVGKQLGADVDFLGTDGCPVRVVKIGLPGGKVKLSGSIS 180
 |||
 DB 246 YVLGVPRMRERPIGDLVVGKQLGADVDFLGTDGCPVRVVKIGLPGGKVKLSGSIS 305
 |||

QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMRFGVKAHSDSMDRPFYIKGQ 240
 |||
 DB 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMRFGVKAHSDSMDRPFYIKGQ 365
 |||

QY 241 KYKSPKNAVVEGDASASVFLAGAAITGGTVVEGGTTSLOGDVKFAVLEMMGAKVTM 300
 |||
 DB 366 KYKSPKNAVVEGDASASVFLAGAAITGGTVVEGGTTSLOGDVKFAVLEMMGAKVTM 425
 |||

QY 301 TETSVTVTGPPQRPFGPKRLKALDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYK 360
 |||
 DB 426 TETSVTVTGPPQRPFGPKRLKALDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYK 485
 |||

QY 361 TERMVAIIRTELTKLASVEEGLDYCIITPEPKLNTAIDTYDDHRMAMFSLAACADV 420
 |||
 DB 486 TERMVAIIRTELTKLASVEEGDPYCIITPEPKLNTAIDTYDDHRMAMFSLAACADV 545
 |||

QY 421 TIRDPGCTRKTFPDYFDVLSTFVK 445
 |||
 DB 546 TIRDPGCTRKTFPDYFDVLSTFVK 570
 |||

RESULT 13
 AAM28463
 ID AAM28463 standard; protein; 444 AA.
 AC AAM28463;
 AC
 DT 17-NOV-1997 (first entry)
 XX
 DE Maize 5-enolpyruvylshikimate-3-phosphate synthase G101A,T102I mutant.
 XX
 KW 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; wild-type; corn;
 KM herbicide tolerance; glyphosate; pRPA-ML-720.
 XX
 OS Zea mays; (strain Black Mexican Sweet).
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 101 /note= "Wild-type Gly has been replaced by Ala"
 FT Misc-difference 102 /note= "Wild-type Thr has been replaced by Ile"
 FT
 XX
 PN MO9704103-A2.
 XX
 PD 06-FEB-1997.
 XX
 PF 18-JUL-1996; 96MO-FR001125.
 XX
 PR 19-JUL-1995; 95FR-00008979.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Lebrun M, Salland A, Freysinet G;

XX MPI, 1997-132642/12.
 DR N-PSDB; AAT86003.
 XX
 PT New mutant gene for 5-enol pyruvylshikimate-3-phosphate synthase -
 PT encodes an enzyme in which Ile replaces Thr at position 102 to give
 PT increased tolerance for glyphosate and related herbicides.
 XX
 PS Claim 9; Page; 26pp; French.
 XX
 CC A 204 bp fragment of the 5-enolpyruvylshikimate-3-phosphate synthase
 CC (EPSPS) gene) was amplified from total DNA of Arabidopsis thaliana (var.
 CC Columbia) using PCR primers having the sequences given in AAT85998 and
 CC AAT85999. Using the amplified fragment as a probe, the wild-type EPSPS
 CC gene was isolated from a maize BMS cDNA library. The EPSPS gene can be
 CC mutated to increase a plant's tolerance to certain herbicides, including
 CC glyphosate. The present sequence represents a specifically claimed
 CC example of a EPSPS double mutant in which the wild-type amino acids at
 CC positions 101 and 102 of the enzyme have been changed by site-directed
 CC mutagenesis of the coding sequence (see features table). Note: this
 CC sequence is not given in the specification but has been created by
 CC modifying the wild-type sequence (AAM28461) as described in example 1
 CC
 XX

SO Sequence 444 AA; 97.0%; Score 2187.5; DB 2; Length 444;
 Query Match Best Local Similarity 97.1%; Pred. No. 3.3e-187;
 Matches 432; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVVKLPGSKLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 60
 |||
 DB 1 AGAEEVVLQPIKISGVVVKLPGSKLSNRIILLSALAEGETTVVDNLNSEDVHYMGLAK 60
 |||

QY 61 TLGLSTEADKAAKRAVAVVCGGKFPVEKDAKEEVOLFLGNAGTAMRSLTAAVTAAGNAT 120
 |||
 DB 61 TLGLSTEADKAAKRAVAVVCGGKFPVE-DAKEEVOLFLGNAGTAMRSLTAAVTAAGNAT 119
 |||

QY 121 YVLGVPRMRERPIGDLVVGKQLGADVDFLGTDGCPVRVVKIGLPGGKVKLSGSIS 180
 |||
 DB 120 YVLGVPRMRERPIGDLVVGKQLGADVDFLGTDGCPVRVVKIGLPGGKVKLSGSIS 179
 |||

QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMRFGVKAHSDSMDRPFYIKGQ 240
 |||
 DB 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMRFGVKAHSDSMDRPFYIKGQ 239
 |||

QY 241 KYKSPKNAVVEGDASASVFLAGAAITGGTVVEGGTTSLOGDVKFAVLEMMGAKVTM 300
 |||
 DB 240 KYKSPKNAVVEGDASASVFLAGAAITGGTVVEGGTTSLOGDVKFAVLEMMGAKVTM 299
 |||

QY 301 TETSVTVTGPPQRPFGPKRLKALDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYK 360
 |||
 DB 300 TETSVTVTGPPQRPFGPKRLKALDVNMNMMPDVAMTLAVVALPADGPTAIRVVASRWYK 359
 |||

QY 361 TERMVAIIRTELTKLASVEEGLDYCIITPEPKLNTAIDTYDDHRMAMFSLAACADV 420
 |||
 DB 360 TERMVAIIRTELTKLASVEEGDPYCIITPEPKLNTAIDTYDDHRMAMFSLAACADV 419
 |||

QY 421 TIRDPGCTRKTFPDYFDVLSTFVK 445
 |||
 DB 420 TIRDPGCTRKTFPDYFDVLSTFVK 444
 |||

RESULT 14
 AAR23065
 ID AAR23065 standard; protein; 444 AA.
 AC AAR23065;
 AC
 DT 22-OCT-1992 (first entry)
 XX
 DE Modified 5-enolpyruvyl-3-phosphoshikimate synthetase (5).
 XX
 KM EPSP; Km; phosphoenolpyruvate; chloroplast; CTP.


```

Db 247 QYLSALIMAAPLALGVIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRPIYKGG 306
Qy 241 KYSPKNAAYVEGDASSAYFLAGAAITGCTVVEGCTTSLQGDVYKPAEVLMMGAKVTW 300
Db 307 KYSPGNAAYVEGDASSAYFLAGAAITGCTVVOGCGTTSLOGDVYKPAEVLMMGAKVTW 366
Qy 301 TETSVTYTGPOREPFGKHLKVIDNNNNKMPDVAMTLAVVALPADGPTAIRDVASNRVKE 360
Db 367 TDTSVTYTGPOREPFGKHLKVIDNNNNKMPDVAMTLAVVALPADGPTAIRDVASNRVKE 426
Qy 361 TERWVAIRTELTKLGASVEEGLDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPV 420
Db 427 TERWVAIRTELTKLGASVEEGDPYCIITPEKLNITALIDTYDDHRMAMAFSLAACADVPV 486
Qy 421 TIRDPGCTRKTFFPYFDVLSFPYKN 445
Db 487 TIRDPGCTRKTFFPYFDVLSFPYKN 511

```

Search completed: September 15, 2005, 14:13:07
 Job time : 175 secs

1995-1996

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2005, 13:57:16 ; Search time 179 Seconds

(Without alignments)
1273.046 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256
Sequence: 1 AGAESEVVLQPIKIKISGVKL.....GCTRKTPPDVLTSPVKN 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing filter 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*
2: uniprot_trcemb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2256	100.0	445	2 095AK1	095AK1 eleusine in
2	2244	99.5	445	2 095AK0	095AK0 eleusine in
3	2199.5	97.5	444	2 024566	024566 zea mays (m
4	2165	96.0	511	2 093VK6	093VK6 oryza sativ
5	1962	87.0	519	2 06BK15	06BK15 conyza cana
6	1949.5	86.4	516	2 0946V0	0946V0 dicliptera
7	1943.5	86.1	516	2 0946U9	0946U9 dicliptera
8	1931	85.6	523	2 06BK14	06BK14 conyza cana
9	1929	85.5	391	2 080428	080428 oryza sativ
10	1927	85.4	516	1 AROA_PETHY	P11043 petunia hyb
11	1911	84.7	516	1 AROA_BRANA	P17688 brassica na
12	1909	84.6	518	2 08W1M5	08W1M5 oryziphrag
13	1897	84.1	521	2 09FV66	09FV66 arabidopsis
14	1896	84.0	514	2 06UDV0	06UDV0 brassica ca
15	1896	84.0	518	1 ARO1_TOBAC	P23981 nicotiana t
16	1893	83.9	521	2 08LC97	08LC97 arabidopsis
17	1888	83.7	520	1 AROA_ARATH	P05466 arabidopsis
18	1879	83.3	454	1 06BKJ3	06BKJ3 conyza cana
19	1877	83.2	530	1 AROA_LYCES	P10748 lycopersico
20	1664	73.8	347	2 09ATJ7	09ATJ7 lolium tigl
21	1597	70.8	358	2 06BK62	06BK62 erigeron an
22	1576	69.9	350	2 06BK61	06BK61 erigeron an
23	1545	68.5	357	2 06BK64	06BK64 amarantus
24	1490	66.0	338	1 ARO2_TOBAC	P23281 nicotiana t
25	1479.5	65.6	330	2 06VH15	06VH15 vitis vinif
26	1459	64.7	331	2 06VVA4	06VVA4 oryza sativ
27	1149	50.9	264	2 06BK60	06BK60 hellantus
28	1147	50.8	265	2 06BK66	06BK66 plantago la
29	1146	50.8	265	2 06BK68	06BK68 sarcocolla
30	1128	50.0	264	2 06BK69	06BK69 hellantus
31	1120.5	49.7	428	2 06BK18	06BK18 yerstinia ps

ALIGNMENTS

32	1119	49.6	428	2 06LPE1	06LPE1 photobacter
33	1118.5	49.6	428	1 AROA_YERPE	060112 yerstinia ps
34	1116	49.5	426	1 AROA_VIBCH	09K800 vibrio chol
35	1115	49.4	426	1 AROA_VIBPA	087QX9 vibrio para
36	1113.5	49.4	427	1 AROA_KLEPN	P24497 klebsiella
37	1113	49.3	428	2 07WJ45	07WJ45 vibrio vuln
38	1113	49.3	456	2 07NTR6	07NTR6 chromobacte
39	1109.5	49.2	427	1 AROA_ECOLI	P07638 escherichia
40	1108	49.1	427	1 AROA_YEREN	P19688 yerstinia en
41	1107.5	49.1	427	1 AROA_SHISO	09ZET7 shigella so
42	1107.5	49.1	427	2 083RY8	083RY8 shigella fl
43	1104.5	49.0	428	2 07NED5	07NED5 photorhabd
44	1103.5	48.9	427	1 AROA_ECOL6	08JH6 escherichia
45	1102.5	48.9	427	1 AROA_SHIDY	087006 shigella dy

RESULT 1

095AK1 ID 095AK1 PRELIMINARY; PRT; 445 AA.

AC 095AK1; 08H1B0; ID 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE 5-enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)

DE (Fragment).

GN Name=epsps-R;

OS Eleusine indica (Goosegrass).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PC/CAD clade; Chloridoideae; Eragrostidae; Eleusine.

OX NCBI_Taxid=29674;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22111118; PubMed=12114580; DOI=10.1104/PP.001560;

RA Baerson S.R., Rodriguez D.J., Tran M., Feng Y., Biebt N.A., Dill G.M.;

RT "Glucose-6-phosphate-resistant goosegrass. Identification of a mutation in the

target enzyme 5-enolpyruvylshikimate-3-phosphate synthase.";

RL Plant Physiol. 129:1265-1275(2002).

RU [2]

RP SEQUENCE FROM N.A.

RX NG C.H., Wickneswari R., Salmijah S., Teng Y.T., Ismail B.S.;

RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.

CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;

CC -1- Sixth step.

CC EMBL; AJ417033; CAD01095.1; -.

DR HSSP; P07638; 1G6S.

DR GO; GO:0003866; F-3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR InterPro; IPR006264; AroA_Ctrnsf.

DR InterPro; IPR001986; EPSP_synth.

DR Pfam; PF00275; EPSP_synthase; 1.

DR ProDom; PD001867; EPSP_synth; 1.

DR TIGRfam; TIGR01356; aroA; 1.

DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.

DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.

KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

Transferase.

FT NON_TER 1 1

SQ SEQUENCE 445 AA; 47403 MW; CACC9BF4632D152F CRC64;

Query Match 100.0%; Score 2256; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 9.7e-147;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	AGAEVVLQJIKELSGVVKLPGSKSLSNKILLLSLAAGTYYVNLNLSDEVHYMLGALK	60
Dd	1 AGAEVVLQJIKELSGVVKLPGSKSLSNKILLLSLAAGTYYVNLNLSDEVHYMLGALK	60
Qy	61 TLGLSVADRAKRAVAVVGGCGKFPVEKDAKEEVLFLGNAGTANRSLTAAVTAAGNAT	120
Dd	61 TLGLSVADRAKRAVAVVGGCGKFPVEKDAKEEVLFLGNAGTANRSLTAAVTAAGNAT	120
Qy	121 YVLIDGVRMERPIGLVYVGLKQLGADVOCPLGTCCPPRKYGTGLPGGRVYKLSGSISS	180
Dd	121 YVLIDGVRMERPIGLVYVGLKQLGADVOCPLGTCCPPRKYGTGLPGGRVYKLSGSISS	180
Qy	181 QYLSALLMAAPLALGDAVEIIEIDKLISIPYEEMTLRLMERFGVKAHSDSMDREYIKGGQ	240
Dd	181 QYLSALLMAAPLALGDAVEIIEIDKLISIPYEEMTLRLMERFGVKAHSDSMDREYIKGGQ	240
Qy	241 KYKSPKNAVYEGDASASVFLAGAAITGCTVTEGCGTTSLOGDVKEFAEVLMMGAVYV	300
Dd	241 KYKSPKNAVYEGDASASVFLAGAAITGCTVTEGCGTTSLOGDVKEFAEVLMMGAVYV	300
Qy	301 TETSVMYTGPOREPFGKHKALIDVNMNMOPVANTLLVALLFDAGPRLIDVASMRVKE	360
Dd	301 TETSVMYTGPOREPFGKHKALIDVNMNMOPVANTLLVALLFDAGPRLIDVASMRVKE	360
Qy	361 TERWVAIRTELTKLGASVEBGLDYCIITPEPKLNTAIDTYDDHRMAVAFSLAACADVPV	420
Dd	361 TERWVAIRTELTKLGASVEBGLDYCIITPEPKLNTAIDTYDDHRMAVAFSLAACADVPV	420
Qy	421 TIRDPGCTRKTCPDYEDULSTPKN	445
Dd	421 TIRDPGCTRKTCPDYEDULSTPKN	445

RESULT 2			
Q95AKO	PRELIMINARY;	PRT;	445 AA.
ID	Q95AKO		
AC	Q95AKO; Q8H1B1;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	5-enolpyruvylshikimate-2,3-phosphate synthase (EC 2.5.1.19)		
DE	(Fragment).		
GN	Name=epsps-S;		
OS	Elaeagnaceae		
CC	Chloroplast		
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
CC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
CC	PACCAD clade; Chloridoideae; Eragrostiidae; Eleusine.		
OX	NCHI_TaxID=29674;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEADLINE=22111148; PubMed=12114580; DOI=10.1104/tp.001560;		
RA	Beeson S.R., Rodriguez D.J., Tren M., Feng Y., Bleet N.A., Dill G.M.;		
RT	"Glucosyltransferase-resistant goosegrass: identification of a mutation in the		
RT	target enzyme 5-enolpyruvylshikimate-3-phosphate synthase.";		
RL	Plant Physiol. 129:1265-1275(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Ng C.H., Wichenawari R., Salimjah S., Teng Y.T., Ismail B.S.;		
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		
CC	phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.		
CC	-1- PATHWAY: Aromatic amino acid biosynthesis; shikimate pathway;		
CC	sixth step.		
CC	-1- SIMILARITY: Belongs to the EPS synthase family.		
DR	EMBL; AJ417034; CADD1096.1; -		
DR	EMBL; AY157642; AAN63155.1; -		
DR	HSSP; P07638; 1G6S		
DR	GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase . . ; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	InterPro; IPR006264; AroA_ctransf.		
DR	InterPro; IPR001986; EPS synth.		

DR pfam; PF00275; Bsp synthase; 1.
DR prodmod; PD00167; Bsp synth; 1.
DR tigrfam; TIGR01356; tca; 1.
DR PROSITE; PS00104; Bsp SYNTHASE_1; 1.
DR PROSITE; PS00885; Bsp SYNTHASE_2; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW transfease; 1
KW NON_TER 1
FT SEQUENCE 445 AA; 47397 MW; 1878975C0925440 CRC64;

Query Match	99.5%	Score 2244;	DB 2;	Length 445;
Best Local Similarity	99.6%	Pred. No. 6.5e-146;		
Matches 443; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	AGAEVLOPIKEIGVYKLPGSKLSNRILLLSALAEGLVDNLLNSEDHYMLGALK	60
Db	1	AGAEVLOPIKEIGVYKLPGSKLSNRILLLSALAEGLTTVDNLLNSEDHYMLGALK	60
Qy	61	TGLSEADKAKARAVVGGCGKPEVEKAEBOVFLGNAGTMRSLTAATPAAGNAT	120
Db	61	TGLSEADKAKARAVVGGCGKPEVEKAEBOVFLGNAGTMRPLTAATPAAGNAT	120
Qy	121	YVLDDGVRRRREPIDGLVYGLKQLGADVDCETLGDPCPPVYKGIIGLPGKRYLSSGIS	180
Db	121	YVLDDGVRRRREPIDGLVYGLKQLGADVDCFLGDCPPVRKKGIGLPGKRYLSSGIS	180
Qy	181	QYLSALIMAAPIALGDVEIEIIDLKLSIPYEMTLRMERFGVAEBHSDSMDFYIKGQ	240
Db	181	QYLSALIMAAPIALGDVEIEIIDLKLSIPYEMTLRMERFGVAEBHSDSMDFYIKGQ	240
Qy	241	KYKSPKNAYVEGDASSASYFLAGAAITGGIYTVEGCGTSLQGDYKFAVLEBMGAKVTW	300
Db	241	KYKSPKNAYVEGDASSASYFLAGAAITGGIYTVEGCGTSLQGDYKFAVLEBMGAKVTW	300
Qy	301	TEKTSVTVGPOREPPGRKHLKAIDVNNMKMPDVMATLAAVALPADGETARIDVASRYKE	360
Db	301	TEKTSVTVGPOREPPGRKHLKAIDVNNMKMPDVMATLAAVALPADGETARIDVASRYKE	360
Qy	361	TERMAVARIETLKLGAASVEBGIDYCIITPEKLNVTADITYDDHRMAAFSLAACADVPE	420
Db	361	TERMAVARIETLKLGAASVEBGIDYCIITPEKLNVTADITYDDHRMAAFSLAACADVPE	420
Qy	421	TIRDBECTRKTPPDYFDVLSTFVN	445
Db	421	TIRDBECTRKTPPDYFDVLSTFVN	445

RESULT 3			
ID	024566	PRELIMINARY;	PRT; 444 AA.
AC	024566;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	3-phosphoshikimate 1-carboxyvinyltransferase (psp-synthase) (EC 2.5.1.19) (Fragment).		
GN	Name=epsr-8;		
OS	Zea mays (Maize).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	PNGCAD clade; Panicoidae; Andropogoneae; Zea.		
OX	NCBI_Taxid=4577;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=BMS;		
RA	Lebrun M., Freysinet M., Sailland A., Rolland A., Freysinet G.;		
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=BMS;		
RA	Lebrun M.C.;		
RL	Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		

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CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acid biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR HMBL; P07638; IM14.
DR GO; GO:0003666; F:3-phosphoshikimate 1-carboxyvinyltransferase. . . ; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . . ; IEA.
DR InterPro; IPR006264; AroA_Ctransf.
DR Pfam; PF00275; EPSP synthase; 1.
DR Prodom; PD001867; EPSP synth; 1.
DR TIGRfam; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW transferase.
SQ SEQUENCE 444 AA; 47282 MW; 30EF0633CC671008 CRC64;

Query Match 97.5%; Score 2199.5; DB 2; Length 444;
Best Local Similarity 97.5%; Pred. No. 7,4e-143;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVLTQPIKEISGVVVKLPGSKSLSNRIILLSALAEQTVVDNLNSDHYVMGLK 60
DB 1 AGAEEVLTQPIKEISGVVVKLPGSKSLSNRIILLSALAEQTVVDNLNSDHYVMGLK 60
QY 61 TLGLSVADKAKRAVAVVGGCGKFPVEKDAKEEVQLFLGNAGTANRSLTAATTAAGNAT 120
DB 61 TLGLSVADKAKRAVAVVGGCGKFPVE-DAKEEVQLFLGNAGTANRSLTAATTAAGNAT 119
QY 121 YVLDGVPNRRERPIGDLVVGKLGADVDVCFLTGDCPPVAVKIGGLPGKVKLSGSIS 180
DB 120 YVLDGVPNRRERPIGDLVVGKLGADVDVCFLTGDCPPVAVVNGIGGLPGKVKLSGSIS 179
QY 181 QYLSALMLAAPLALGDVEIRIIDLKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 240
DB 180 QYLSALMLAAPLALGDVEIRIIDLKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASASVFLAGAITGTVVGGCTTSLQGDVFAEVLMMGAKVTM 300
DB 240 KYKSPKNAVVEGDASASVFLAGAITGTVVGGCTTSLQGDVFAEVLMMGAKVTM 299
QY 301 TETSVTVTGPOREPFGKRLKALIDVNMKNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
DB 300 TETSVTVTGPOREPFGKRLKALIDVNMKNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 359
QY 361 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 420
DB 360 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 419
QY 421 TIRDPGCTRKTFPDYFDVLSFTVKN 445
DB 420 TIRDPGCTRKTFPDYFDVLSFTVKN 444

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RN [1]
RN SEQUENCE FROM N.A.
RA Wu L., Nagano H., Yoshida K., Kawaasaki S., Kishima Y., Sano Y.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Wang X.J., Jiang F.D., Gang L.X., Zhen Z.;
RT Chromosome location.
RT "Isolation and characterization of rice EPSP synthase and its
RN Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 0:0-0(2001).
RN [3]
RN SEQUENCE FROM N.A.
RA Wang X.J., Zhen Z.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL; AB052962; BAB61062.1; -.
DR EMBL; AF413081; AAL06593.1; -.
DR EMBL; AF413082; AAL07437.1; -.
DR HSSP; P07638; 1G6S.
DR Gramene; Q93VK6; -.
DR GO; GO:0003666; F:3-phosphoshikimate 1-carboxyvinyltransferase. . . ; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . . ; IEA.
DR InterPro; IPR006264; AroA_Ctransf.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR Prodom; PD001867; EPSP synth; 1.
DR TIGRfam; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW transferase.
SQ SEQUENCE 511 AA; 53971 MW; A4265CB513C840AB CRC64;

Query Match 96.0%; Score 2165; DB 2; Length 511;
Best Local Similarity 95.1%; Pred. No. 2e-140;
Matches 423; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 AGAEEVLTQPIKEISGVVVKLPGSKSLSNRIILLSALAEQTVVDNLNSDHYVMGLK 60
DB 67 AGAEEVLTQPIKEISGVVVKLPGSKSLSNRIILLSALAEQTVVDNLNSDHYVMGLK 126
QY 61 TLGLSVADKAKRAVAVVGGCGKFPVEKDAKEEVQLFLGNAGTANRSLTAATTAAGNAT 120
DB 127 ALGLSVADKAKRAVAVVGGCGKFPVEKDAKEEVQLFLGNAGTANRSLTAATTAAGNAT 186
QY 121 YVLDGVPNRRERPIGDLVVGKLGADVDVCFLTGDCPPVAVKIGGLPGKVKLSGSIS 180
DB 187 YVLDGVPNRRERPIGDLVVGKLGADVDVCFLTGDCPPVAVVNGIGGLPGKVKLSGSIS 246
QY 181 QYLSALMLAAPLALGDVEIRIIDLKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 240
DB 247 QYLSALMLAAPLALGDVEIRIIDLKLSIPYEMTLRLMERFGVKAHSDSMDRFYIKGQ 306
QY 241 KYKSPKNAVVEGDASASVFLAGAITGTVVGGCTTSLQGDVFAEVLMMGAKVTM 300
DB 307 KYKSPKNAVVEGDASASVFLAGAITGTVVGGCTTSLQGDVFAEVLMMGAKVTM 366
QY 301 TETSVTVTGPOREPFGKRLKALIDVNMKNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
DB 367 TETSVTVTGPOREPFGKRLKALIDVNMKNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 426
QY 361 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 420
DB 427 TERMAVAIRTELTKGASVEBGIDYCIITPEKLNATRIDYDDHMAAFSLAACADVPV 486
QY 421 TIRDPGCTRKTFPDYFDVLSFTVKN 445
DB 487 TIRDPGCTRKTFPDYFDVLSFTVKN 511

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RESULT 5
ID Q6B6L5 PRELIMINARY; PRT; 519 AA.
AC Q6B6L5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 5-enol-pyruvylshikimate-phosphate synthase.
GN Name=EPSPS1.
OS Conyza canadensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asteroideae; Astereae; Conyza.
OX NCBI_TaxId=72917;
RN [1]
RP SEQUENCE FROM N.A.
RA Heck G.R., Alibhai M., Hubmeier C.S., Flaesink S., Malven M., Qi Y.,
RA Chen Y.-C.S., Bunkers G.J., Sammons R.D., Feng P.C.C., Foadey W.T.,
RA Cadzow C.A.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL: AY545666; AF45243.1; -
DR GO: GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
DR GO: GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
DR InterPro: IPR006264; ArcoA.Ctrnsf.
DR InterPro: IPR001986; EPSP synth.
DR Pfam: PF00275; EPSP synthase; 1.
DR Prodom: PD001867; EPSP synth; 1.
DR TIGRfam: TIGR01356; aroA. 1.
DR PROSITE: PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE: PS00885; EPSP SYNTHASE_2; 1.
DR KMW: Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
DR Transferrase.
SQ SEQUENCE 519 AA; 55210 MW; 47FE6706C8CDBE3 CRC64;

Query Match 87.0%; Score 1962; DB 2; Length 519;
Best Local Similarity 85.5%; Pred. No. 1.8e-126;
Matches 377; Conservative 34; Mismatches 30; Indels 0; Gaps 0;

QY 5 EYVLQPIKEISGVVYKLGSGKSLNSNRILLSLAEGTTVDNLSBDVHYMLGALTKTGL 64
DB 79 EYVLQPIKEISGVVYKLGSGKSLNSNRILLSLAEGTTVDNLSBDVHYMLGALTKTGL 138
QY 65 SYEADKAARAAVAVVCGGKFEVKEKAEVOLFLNAGTAMRSLTAAVTAAGNATYYLD 124
DB 139 NVEEDVAIKRAIVGGGVPVPGKAKNDIQFLNAGTAMRPLTAAVTAAGNATYYLD 198
QY 125 GVPNRERRPIGLVYGLKQLGADVDCFLGTCPPVRYKIGLPGKRYKLSGSSISQYIS 184
DB 199 GVPNRERRPIGLVYGLKQLGADVDCFLGTCPPVRYKIGLPGKRYKLSGSSISQYIS 258
QY 185 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRPFYIKGGQKYKS 244
DB 259 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRPFYIKGGQKYKS 318
QY 245 PKNAAYVEGDASASAYFLAGAAITGGTIVYVCGGTSISLOGDVYFAVLEMGAKVWTETS 304
DB 319 PKNAAYVEGDASASAYFLAGAAITGGTIVYVCGGTSISLOGDVYFAVLEMGAKVWTETS 378
QY 305 VYVYTGPOREPFGRKHLKALIDVNMNMKPDVAMTLAAVVALPADGPTAIRDVASRWVETERN 364
DB 379 VYVYTGPOREPFGRKHLKALIDVNMNMKPDVAMTLAAVVALPADGPTAIRDVASRWVETERN 438
QY 365 VAIRTELTKGASVEGLDYCIITPPEKLVNTAIDTYDHRMMAAISLAACAVPTIID 424
DB 439 IALCTELRKGAIVBEGPDYCVIITPPEKLVNTAIDTYDHRMMAAISLAACAVPTIID 498

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QY 425 PGCTRKTPDYEDVLSTFVKN 445
DB 499 PGCTRKTPDYEDVLSTFVKN 519

RESULT 6
ID Q946V0 PRELIMINARY; PRT; 516 AA.
AC Q946V0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 5-enolpyruvylshikimate-3-phosphate synthase.
OS Dicotyledonae;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Acanthaceae; Acanthoideae; Ruellieae; Dufouciaceae;
OC Dicotyledonae.
OX NCBI_TaxId=173162;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan C.T., Chiang M.Y., Chen Y.M.;
RT "Triple mechanisms of glyphosate-resistance in a naturally occurring
RT glyphosate-resistant plant Dicliptera chinensis."
RL Plant Sci. 163:543-554(2002).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL: AF371965; AL27697.1; -
DR HSSP: P07638; 1G6S.
DR GO: GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
DR InterPro: IPR006264; ArcoA.Ctrnsf.
DR InterPro: IPR001986; EPSP synth.
DR Pfam: PF00275; EPSP synthase; 1.
DR Prodom: PD001867; EPSP synth; 1.
DR TIGRfam: TIGR01356; aroA. 1.
DR PROSITE: PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE: PS00885; EPSP SYNTHASE_2; 1.
DR KMW: Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
DR Transferrase.
SQ SEQUENCE 516 AA; 54913 MW; B8C1396F0F1D2D18 CRC64;

Query Match 86.4%; Score 1949.5; DB 2; Length 516;
Best Local Similarity 85.6%; Pred. No. 1.3e-125;
Matches 375; Conservative 37; Mismatches 25; Indels 1; Gaps 1;

QY 5 EYVLQPIKEISGVVYKLGSGKSLNSNRILLSLAEGTTVDNLSBDVHYMLGALTKTGL 64
DB 77 EYVLQPIKEISGVVYKLGSGKSLNSNRILLSLAEGTTVDNLSBDVHYMLGALTKTGL 136
QY 65 SYEADKAARAAVAVVCGGKFEVKEKAEVOLFLNAGTAMRSLTAAVTAAGNATYYLD 124
DB 137 AVEEDKAARAAVAVVCGGKFEVKEKAEVOLFLNAGTAMRPLTAAVTAAGNATYYLD 196
QY 125 GVPNRERRPIGLVYGLKQLGADVDCFLGTCPPVRYKIGLPGKRYKLSGSSISQYIS 184
DB 197 GVPNRERRPIGLVYGLKQLGADVDCFLGTCPPVRYKIGLPGKRYKLSGSSISQYIS 256
QY 185 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRPFYIKGGQKYKS 244
DB 257 ALMAAPALAGDVEIEIIDLKISIPYEMTLRLMERPGVKAHSDMDRPFYIKGGQKYKS 316
QY 245 PKNAAYVEGDASASAYFLAGAAITGGTIVYVCGGTSISLOGDVYFAVLEMGAKVWTETS 304
DB 317 PKNAAYVEGDASASAYFLAGAAITGGTIVYVCGGTSISLOGDVYFAVLEMGAKVWTETS 376
QY 305 VYVYTGPOREPFGRKHLKALIDVNMNMKPDVAMTLAAVVALPADGPTAIRDVASRWVETERN 364
DB 377 VYVYTGPOREPFGRKHLKALIDVNMNMKPDVAMTLAAVVALPADGPTAIRDVASRWVETERN 435

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QY	305	VVTYTGQREBFGRKHLKAIADVMNTQPDVAMTLAVVALPADGPALINDVASMRVKTETERM	364
DB	377	VVTGTPPRVP-GKKHLRAIDVMNMQMPVAMTLAVVALPADGPALINDVASMRVKTETERM	435
QY	365	VAIRTELTKLGSVVEGDLDCITTEPEKANTALIDTYDDHNMMAFSLAACADVPVIR	424
DB	436	IAICTELRKLGAIVEGDPYCIITPEKLANVALDITDDHNMMAFSLAACADVPVIRK	495
QY	425	PGCTRKTFPDYDVLSTP 442	
DB	496	PGCTRKTFPDYDVLSTY 513	
RESULT 8			
Q6E6I4			
AC	Q6E6I4	PRELIMINARY; PRT; 523 AA.	
DT	25-OCT-2004 (TEMBLrel. 28, Created)		
DT	25-OCT-2004 (TEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TEMBLrel. 28, Last annotation update)		
DE	5-enol-pyruvylshikimate-phosphate synthase.		
GN	Name=EPSPS2;		
OS	Conyza canadensis.		
OC	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	campanulales; Asterales; Asteraceae; Asteroideae; Astereae; Conyza.		
OX	NCBI_TaxId=72917;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Heck G.-R., Alibhai M., Hubmeier C.S., Plasinski S., Malven M., Qi Y.,		
RA	Chen Y.-C.S., Bunkers G.J., Sammons R.D., Feng P.-C.C., Foadey W.T.,		
RA	Chacob C.A.;		
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		
CC	phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.		
CC	-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;		
CC	sixth step.		
CC	-1- SIMILARITY: Belongs to the EPSP synthase family.		
DR	EMBL; AY545667; AAT5244.1; .		
DR	GO; GO:0003866; P.3-phosphoshikimate 1-carboxyvinyltransferase. . ; IEA.		
DR	GO; GO:0016089; P. aromatic amino acid family biosynthesis. sh. . ; IEA.		
DR	InterPro; IPR006264; AroA Transf.		
DR	InterPro; IPR001986; EPSP_synth.		
DR	Pfam; PF00275; EPSP_synthase; 1.		
DR	Prodom; PD001867; EPSP_synth; 1.		
DR	TIGRFAMs; TIGR01356; aroA; 1.		
DR	PROSITE; PS00104; EPSP SYNTHASE 1; 1.		
DR	PROSITE; PS00885; EPSP SYNTHASE 2; 1.		
KM	Amino acid biosynthesis; Aromatic amino acid biosynthesis;		
KM	Transferase.		
SW	SEQUENCE 523 AA; 55811 MW; 24B2799B042D95F6 CRC64;		
Query Match 85.6%; Score 1931; DB 2; Length 523;			
Best Local Similarity 83.5%; Pred. No. 2,5e-124;			
Matches 365; Conservative 40; Mismatches 33; Indels 0; Gaps 0			
QY	4	EEVVLQPIKEISGVVKLPGSKSLNSRILLLSALAEAGTTVDNLINSEDVHYMLGALKTIG 63	
DB	82	EEIVLQPIQISGTVHLPGSKSLNSRILLLSALAEAGTTVDNLINSDVHYMLGALRALG 141	
QY	64	LSVLEADKAKAVVVGCCGKPPVEVDAAEYQLTGNAAGTAMSLTAATVAAGNATVYL 123	
DB	142	LNVESNAISAKRAIVGCGGVFPVVGKADRIQLFLGNAAGTAMRPLTAATVAAGNSSYLL 201	
QY	124	DGVPRRREKRPIDLVVGKQKLGADVDCFLGTDCPPVVKIGIGLPGGKVLGSGISSQYL 183	
DB	202	DGVPRRREKRPIDLVITGLKQKLGAVNDCSLGNCPPAVVVGSGGLPGGKVLGSSISSQYL 261	
QY	184	SALLMAAPLALGDVEIIRIIDLKILSIPVEMTLRLMERPGYKAHSHSDWRFYIKGQKTX 243	
DB	262	TSLTMAAPALALGDVEIIRIIDLKILSIPVYEMTLRLMERFGVSVSHSDWRFHVRGQKTX 321	

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QY 244 SPKNAYVEGDASASFLAGAAITGGTVVEGGCTTSLQGDVFAEVLBNMGAQVWTET 303
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 322 SPENAYVEGDASASFLAGAAITGGTVVEGGCTTSLQGDVFAEVLBNMGAQVWTEN 381
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 304 SVTVTGPQEPFPRKRLKALIDVNMNMKPDVAMTLAVVALPADGPTAIRDVAHRYKETER 363
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 382 SVTVKPPRRSSGRGHLRPVDVNMNMKPDVAMTLAVVALYADGPTAIRDVAHRYKETER 441
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 364 MVAIRTELTLGASVEBGLDYCIITPPEKLNVAITDYPDHRMAMAFLAACADVPVTR 423
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 442 MINICTELKRLGATVEBGPDIYITPPEKLNVAITDYPDHRMAMAFLAACADVPVTR 501
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 424 DPCTRKTPEPDYFDVLTFTVKN 445
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 502 DPCTRKTPEPDYFDVLTFTVKN 523
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ID 080428 PRELIMINARY; PRT; 391 AA.
AC 080428;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase.
GN Name=epsp-8; Synonyms=P0679C08.29;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaraloideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=T65wx;
RA Kishima Y., Sano Y.;
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC CC SIMILARITY: Belongs to the EPSP synthase family.
DB EMBL: AB016765; BAA32376.1; -.
DB HSSP: P07638; 1G6S.
DR Gramene; O80428; -.
DR GO: GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. .; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0016089; P:aromatic amino acid family biosynthesis, sh. .; IEA.
DR InterPro: IPR006264; AroC Ctransf.
DR InterPro: IPR001986; EPSP_synth.
DR Pfam: PF00275; EPSP_synthase; 1.
DR ProDom: PD001867; EPSP_synth; 1.
DR TIGRPFAM: TIGR01356; aroC; 1.
DR PROSITE: PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE: PS00885; EPSP_SYNTHASE_2; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW transferase.
SQ SEQUENCE 391 AA; 41709 MW; CB3FL7C39F30ACBD CRC64;

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Query Match 85.5%; Score 1929; DB 2; Length 391;
Best Local Similarity 95.9%; Pred. No. 2.4e-124;
Matches 375; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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QY 55 MGLALTLGLSVADRAKRAVVVGGGKPEVEKDAKEVQLFLGAGTAMSLTAAYTA 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGLALTLGLSVADRAKRAVVVGGGKPEVEKDAKEVQLFLGAGTAMRLTAAYTA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 AGGNATVYLDGVRMRBRPIGDLVVLKQLGADVDFLTGDCPPVAVKIGLPGKRVTL 174
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 61 AGGNATVYLDGVRMRBRPIGDLVVLKQLGADVDFLTGDCPPVAVKIGLPGKRVTL 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 SSSISQVLSALIMAPLADGVEIETDKLISIPYEMTLKMRFGVKAHSDSWDRF 234
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 SSSISQVLSALIMAPLADGVEIETDKLISIPYEMTLKMRFGVKAHSDSWDRF 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 235 YIKGQKYSPPKNAYVEGDASASFLAGAAITGGTVVEGGCTTSLQGDVFAEVLBNM 294
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 YIKGQKYSPPKNAYVEGDASASFLAGAAITGGTVVEGGCTTSLQGDVFAEVLBNM 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 295 GAKVTWTSTVTVTGPQEPFPRKRLKALIDVNMNMKPDVAMTLAVVALPADGPTAIRDVA 354
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 GAKVTWTSTVTVTGPQEPFPRKRLKALIDVNMNMKPDVAMTLAVVALPADGPTAIRDVA 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 355 SMRYKETERMVAIRTELTLGASVEBGLDYCIITPPEKLNVAITDYPDHRMAMAFLAA 414
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 SMRYKETERMVAIRTELTLGASVEBGLDYCIITPPEKLNVAITDYPDHRMAMAFLAA 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 415 CADVPVTRIDPCTRKTPEPDYFDVLTFTVKN 445
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 CADVPVTRIDPCTRKTPEPDYFDVLTFTVKN 391
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
ID AROA_PETHY STANDARD; PRT; 516 AA.
AC P11043;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase, chloroplast precursor
DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (Epsp
DE synthase).
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Mitchell;
RX MEDLINE=88153749; PubMed=3346248;
RA Gasser C.S., Winter J.A., Hironaka C.M., Shah D.M.;
RT "Structure, expression, and evolution of the 5-enolpyruvylshikimate-3-
RT phosphate synthase genes of petunia and tomato.";
RL J. Biol. Chem. 263:4280-4289(1988).
RN [2]
RX MUTAGENESIS OF GLY-173.
RX MEDLINE=92042175; PubMed=1939260;
RA Padgett S.R., Re D.B., Gasser C.S., Eicholtz D.A., Frazier R.B.,
RA Hironaka C.M., Levine E.B., Shah D.M., Fraley R.T., Kishore G.M.;
RT "Site-directed mutagenesis of a conserved region of the 5-
RT enolpyruvylshikimate-3-phosphate synthase active site.";
RL J. Biol. Chem. 266:22364-22369(1991).
CC -1- CATALYTIC ACTIVITY: phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC CC SUBCELLULAR LOCATION: Chloroplast.
CC -1- MISCELLANEOUS: This enzyme is the target of the potent, broad-
CC spectrum herbicide, glyphosate [n-(phosphonomethyl)glycine].
CC Overproduction of EPSP leads to glyphosate tolerance.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
DB EMBL: M21084; AAA33699.1; -.

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DR PIR; A28198; XUPJVS.
 DR HSSP; P07638; 1G6S.
 DR InterPro; IPR006264; AroA.
 DR InterPro; IPR001986; Epsp_synth.
 DR Pfam; PF00275; Epsp_synthase; 1.
 DR ProDom; PD001867; Epsp_synth; 1.
 DR TRIGRAM; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; Epsp_SYNTHASE_1; 1.
 DR PROSITE; PS00885; Epsp_SYNTHASE_2; 1.
 DR Aromatic amino acid biosynthesis; Chloroplast; Herbicide resistance;
 KM Transferrase; Transf. peptide.
 FT TRANSIT 1 72 Chloroplast.
 FT CHAIN 73 516 carboxyvinyltransferase.
 FT MUTAGEN 173 173 G-A: Resistance to glyphosate.
 SQ SEQUENCE 516 AA; 55537 MW; 1A753E717BE7BAF8 CRC64;
 Query Match 85.4%; Score 1927; DB 1; Length 516;
 Best Local Similarity 84.4%; Pred. No. 4,6e-124;
 Matches 372; Conservative 31; Mismatches 38; Indels 0; Gaps 0;
 QY 5 EVVLQPIKEISGVVGLPGSKSLNRIILLALAEETTVDNLINSEVHYMLGALKTLGL 64
 DB 76 EIVLQPIKEISGVVGLPGSKSLNRIILLALAEETTVDNLINSDIHMYLGLTKTLGL 135
 QY 65 SVKADKAAKAAVAVVGGCGKFPVKKAKKEVQLFLGNAAGTMRSLTAATPAAGNATVVD 124
 DB 136 HVEEDSANQRAVVEGGGGLFPVKEKEKEIQLFLGNAAGTMRPLTAATVVAAGNSRYVD 195
 QY 125 GVPKMERPIGDLVGLKQLGADVDFLTGDCPPVVKIGLPGGKVLGSGISSQYLS 184
 DB 196 GVPKMERPIGDLVGLKQLGADVDFLTGDCPPVVKIVSGGLPGGKVLGSGISSQYLT 255
 QY 185 ALIAPALAGDVEIEIIDKLISIPYEMTLRLMERFGVAEHSDSMDRPFYIKGGQKYS 244
 DB 256 ALIAPALAGDVEIEIIDKLISIPYEMTLRLMERFGISVEHSDSMDRPFVAGQKYS 315
 QY 245 PKAAVVEGDASSSYFLAGAAITGGVTVVGGCTTSLQGVKAEVLEKMGAGVTTTTS 304
 DB 316 PKAAVVEGDASSSYFLAGAAITGGVTVVGGCTTSLQGVKAEVLEKMGAGVTTTTS 375
 QY 305 VVTVGQREPPFGKHLKALIDVNNKMPDVAMTLAAVVALPADGPTAIRDVASMKVETEM 364
 DB 376 VVTVGQREPPFGKHLKALIDVNNKMPDVAMTLAAVVALPADGPTAIRDVASMKVETEM 435
 QY 365 VAIKTELTKLGASVEBGLDLCITTPPEKLVNTAIDTYDDHRMAAFSLAACADVPYTI 424
 DB 436 VAIKTELTKLGASVEBGLDLCITTPPEKLVNTAIDTYDDHRMAAFSLAACADVPYTI 495
 QY 425 PGCTRTKTPPYFDVLSTFVN 445
 DB 496 PGCTRTKTPPYFDVLSTFVN 516
 RESULT 11
 AROA_BRANA STANDARD; PRT; 516 AA.
 ID AROA_BRANA STANDARD; PRT; 516 AA.
 AC P17688;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase, chloroplast precursor
 DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (Epsp
 synthase).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroside II; Brassicales; Brassicaceae; Brassica.
 OK NCBI_TaxId=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Westar;
 RX MEDLINE=90251470; PubMed=2339069;

RA Gasser C.S., Klee H.J.;
 "A Brassica napus gene encoding 5-enolpyruvylshikimate-3-phosphate
 synthase."
 RL Nucleic Acids Res. 18:2821-2821 (1990).
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- MISCELLANEOUS: This enzyme is the target of the potent, broad-
 CC spectrum herbicide, glyphosate [n-(phosphonomethyl)glycine].
 CC Overproduction of Epsp leads to glyphosate tolerance.
 CC -1- SIMILARITY: Belongs to the Epsp synthase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X51475; CAA35839.1; -.
 DR PIR; S12744; S12744.
 DR HSSP; P07638; 1G6S.
 DR InterPro; IPR006264; AroA.
 DR InterPro; IPR001986; Epsp_synth.
 DR Pfam; PF00275; Epsp_synthase; 1.
 DR ProDom; PD001867; Epsp_synth; 1.
 DR TRIGRAM; TIGR01356; aroA; 1.
 DR PROSITE; PS00104; Epsp_SYNTHASE_1; 1.
 DR PROSITE; PS00885; Epsp_SYNTHASE_2; 1.
 DR Aromatic amino acid biosynthesis; Chloroplast; Transferrase;
 KM Transf. peptide.
 FT TRANSIT 1 72 Chloroplast (potential).
 FT CHAIN 73 516 carboxyvinyltransferase.
 FT SEQUENCE 516 AA; 55030 MW; 86804B4BD8D0F57 CRC64;
 Query Match 84.7%; Score 1911; DB 1; Length 516;
 Best Local Similarity 82.8%; Pred. No. 5.8e-123;
 Matches 367; Conservative 35; Mismatches 41; Indels 0; Gaps 0;
 QY 3 AEEVVLQPIKEISGVVGLPGSKSLNRIILLALAEETTVDNLINSEVHYMLGALKTL 62
 DB 74 AEEVVLQPIKEISGVVGLPGSKSLNRIILLALAEETTVDNLINSDIHMYLGLTKTLGL 133
 QY 63 GSVEADKAAKAAVAVVGGCGKFPVKKAKKEVQLFLGNAAGTMRSLTAATPAAGNATV 122
 DB 134 GSVKADKAAKAAVAVVGGCGGGLFPVKEKEKEIQLFLGNAAGTMRPLTAATVVAAGNSRY 193
 QY 123 LDGVPKMERPIGDLVGLKQLGADVDFLTGDCPPVVKIGLPGGKVLGSGISSQY 182
 DB 194 LDGVPKMERPIGDLVGLKQLGADVDFLTGDCPPVVKIVSGGLPGGKVLGSGISSQY 253
 QY 183 LSALLMAAPALAGDVEIEIIDKLISIPYEMTLRLMERFGVAEHSDSMDRPFYIKGGQY 242
 DB 254 LSALLMAAPALAGDVEIEIIDKLISIPYEMTLRLMERFGVAEHSDSMDRPFVAGQY 313
 QY 243 KSPKAAVVEGDASSSYFLAGAAITGGVTVVGGCTTSLQGVKAEVLEKMGAGVTTTTS 302
 DB 314 KSPKAAVVEGDASSSYFLAGAAITGGVTVVGGCTTSLQGVKAEVLEKMGAGVTTTTS 373
 QY 303 TSVTVTGQREPPFGKHLKALIDVNNKMPDVAMTLAAVVALPADGPTAIRDVASMKVETE 362
 DB 374 TSVTVTGQREPPFGKHLKALIDVNNKMPDVAMTLAAVVALPADGPTAIRDVASMKVETE 433
 QY 363 RVVAIRTELTKLGASVEBGLDLCITTPPEKLVNTAIDTYDDHRMAAFSLAACADVPYTI 422
 DB 434 RVVAIRTELTKLGASVEBGLDLCITTPPEKLVNTAIDTYDDHRMAAFSLAACADVPYTI 493
 QY 423 RDPGCTRTKTPPYFDVLSTFVN 445
 DB 493 RDPGCTRTKTPPYFDVLSTFVN 516

Db 494 KDBGCTRKTPDPYFQVLESITKH 516

RESULT 12

OB81M5 PRELIMINARY; PRT; 518 AA.

AC 081M5; 01-MAR-2002 (TEMBLrel. 20, Created)

DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)

DE 5-enolpyruvylshikimate-3-phosphate synthase.

OS Oryctolagus cuniculus.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Orychophragmus.

NCBI_TaxId=71234;

OX [1]

RP SEQUENCE FROM N.A.

RA Lin X.-F., Liu X.-J., Gou X.-S., Gao H., Deng Y.-T.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Liu X.-J., Deng Y.-T., Gao H., Gou X.-S., Wu J., Li X.-F.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

CC -1- PHOSPHATE + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.

CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;

CC sixth step.

CC -1- SIMILARITY: Belongs to the EPSP synthase family.

DR EMBL; AF440389; AAL65913.1; -.

DR HSP; P07638; I668.

DR GO; GO:0003666; P:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.

DR GO; GO:0016740; P:transferase activity; IEA.

DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.

DR Pfam; PF00275; EPSP synthase; 1.

DR Prodom; PD001867; EPSP_synth; 1.

DR TrIRFam; TIRG01356; aroA; 1.

DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.

DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.

KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

KW Transferase

SO SEQUENCE 518 AA; 55292 MW; 75C16733F594B0E0 CRC64;

Query Match 84.6%; Score 1909; DB 2; Length 518;

.Best Local Similarity 82.8%; Pred. No. 8e-123;

Matches 367; Conservative 35; Mismatches 41; Indels 0; Gaps 0;

QY 3 AEEVTLQPIKEIGGVKLPSSKLSNRILLLSALABSTTVVDNLNSEDVHYMLGALKTL 62

DB 76 ASEIVLQPIKEISGLIKLPSSKLSNRILLLSALABSTTVVDNLNSEDVHYMLGALKTL 135

QY 63 GLSEADKAKRAVAVVVGCGKPFVEQAKREVLPIGNATARSITAAATAAGNATY 122

DB 136 GLNVERDSNNRVAVBGGGIFPASVDSKSDIEVLGNATARRPLAATAAGNASTY 195

QY 123 LDGVPNRERRPIDLVGLKQLGADVDFLTGDCPPRVKIGIGLPGKVKLSGSISSQY 182

DB 196 LDGVPNRERRPIDLVGLKQLGADVDFLTGDCPPRVKIGIGLPGKVKLSGSISSQY 255

QY 183 LSLALMAAPLADVEIEITDKLISIFYEMTILMERFVYKAHSDSDRPITKGGQKY 242

DB 256 LTLALMAAPLADVEIEITDKLISIFYEMTILMERFVYKAHSDSDRPITKGGQKY 315

QY 243 KSPKNAVVEGDASSASYFLAGAILTGTVVVGCGTSLGQDVKPFVEMMAKATYTW 302

DB 316 KSPKNAVVEGDASSASYFLAGAILTGTVVVGCGTSLGQDVKPFVEMMAKATYTW 375

QY 303 TSVTVGPQREPFGRKILKAIQVNMKMPVAMTLAVALLADGPAIRDVAGSRVETE 362

DB 376 NSVTVGPQREPFGRKILKAIQVNMKMPVAMTLAVALLADGPAIRDVAGSRVETE 435

QY 363 RMVAIRTELTKLQASVEEGIDYCIITPPEKLVNTAIDTYDHRMAAFSLAACADVPVTI 422

Db 436 RMAIALCTELRKLGATVEBGSDYCVITPPAKVPAEIDTYDHRMAAFSLAACADVPVTI 495

QY 423 RDBGCTRKTPDPYFQVLESITKH 445

Db 496 KDBGCTRKTPDPYFQVLESITKH 518

RESULT 13

Q9FVP6 PRELIMINARY; PRT; 521 AA.

AC 09FVP6; 01-MAR-2001 (TEMBLrel. 16, Created)

DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)

DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, putative (Putative 3-phosphate, putative).

GN Name=F27K7.11; Synonym=At1g48860, T24P22.2;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxId=3702;

OX [1]

RP SEQUENCE FROM N.A.

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Egeu P., Lee J.M.,

RA Toriumi M., Yu G., Brooks S., Chao O., Chen H., Karlin-Neumann G.,

RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shin P.,

RA Southwick A., Davis R.W., Ecker J.R., Theologis A.,

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RA Malet R., Rönning C.M., Koo H., Fujii C.Y., Utecherback T.R.,

RA Barnstead M.E., Bowman C.L., White O., Niernan W.C., Frazer C.M.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

RA Carrinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamaya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.,

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =

CC -1- PHOSPHATE + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.

CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;

CC sixth step.

CC -1- SIMILARITY: Belongs to the EPSP synthase family.

DR EMBL; AC084414; AAG29739.1; -.

DR EMBL; AY040065; AAK64123.1; -.

DR EMBL; AC084242; AAG50661.1; -.

DR EMBL; AF360224; AAK25934.1; -.

DR PIR; D96526; D96526.

DR HSP; P07638; I668.

DR GO; GO:0003866; P:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.

DR GO; GO:0016740; P:transferase activity; IEA.

DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.

DR InterPro; IPR006264; AroA_citnsf.

DR InterPro; IPR001986; EPSP synth.

DR Pfam; PF00275; EPSP synthase; 1.

DR Prodom; PD001867; EPSP_synth; 1.

DR TrIRFam; TIRG01356; aroA; 1.

DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.

DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.

KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KM Transferrase.
SQ SEQUENCE 521 AA; 55831 MW; E2AB525FCE1AC7 CRC64;

Query Match 84.1%; Score 1897; DB 2; Length 521;
Best Local Similarity 82.2%; Pred. No. 5,4e-122;
Matches 364; Conservative 36; Mismatches 43; Indels 0; Gaps 0;

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QY 3 AEEVVLQPIKEISGVKLPKSGKSLSNRIILLALAEITVVDNLNSEDVHYMLGALKTL 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 ASIVVQLPIRQISGLIKLPKSGKSLSNRIILLALAEITVVDNLNSEDVHYMLGALKTL 138
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 GLSVEADKAKRAVAVVCGCGKPFVEKDAKEVQLFLGNAGTAMRSITLAATAAGNATYV 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 GLNVERHSENNRAVVEGCGVFPASIDSKSDIELYGNAGTAMRPLTAATAAGNATYV 198
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 LDGVPFMRERPIGDLVVGKQLGADVDCFLGDCPPVRVXGIGLPKGVKLSGSISSQY 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 199 LDGVPFMRERPIGDLVVGKQLGADVDCFLGDCPPVRVXGIGLPKGVKLSGSISSQY 258
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 LSAALMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVKAHSDSDMRFFVKGQKY 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 259 LTRALLMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVKAHSDSDMRFFVKGQKY 318
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 KSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLQGVKFAVLEMMGAKYTWTE 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 319 KSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLQGVKFAVLEMMGAKYTWTE 378
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 TSVTVTGPOREPFGKRLKALIDVNMNMKPDVAMTLAVALFADGPTAIRDVASWRKYETE 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 379 NSVTYVGPBRDAFGMRLRAIDVNMNMKPDVAMTLAVALFADGPTAIRDVASWRKYETE 438
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 363 RMAVITELTKLGAASVEEGDLCITPPEKLANVTAIDTDDHMMMAFSLAACADVPVIT 422
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 439 RMAVITELTKLGAATVEEGSDYCVITPPKVPKPAEIDTDDHMMMAFSLAACADVPVIT 498
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 423 RDGCTRKTFPDYFDVLTSTFVN 445
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 499 NDGCTRKTFPDYFDVLEIRTKH 521
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 14

Q6JDV0 PRELIMINARY; PRT; 514 AA.
AC Q6JDV0,
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ID 5-enolpyruvylshikimate-3-phosphate synthase.
GN Name=EPSP,
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA You D., Qian Y., Li X.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
DR EMBL; AY512663; AA680163.1; -;
DR GO; GO:0003866; F:3-phosphoshikimate-1-carboxyvinyltransferase. . .; IEA.
DR GO; GO:0016740; F:aromatase activity; IEA.
DR GO; GO:0016089; P:aromatase amino acid family biosynthesis, sh. . .; IEA.
DR InterPro; IPR006264; AroA Ctranaef.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR ProDom; PD001867; EPSP_synth; 1.

DR TIGRPA6; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.
KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KM Transferrase.
SQ SEQUENCE 514 AA; 55113 MW; ACTADCB8FDAB0301 CRC64;

Query Match 84.0%; Score 1896; DB 2; Length 514;
Best Local Similarity 82.2%; Pred. No. 6,2e-122;
Matches 364; Conservative 37; Mismatches 42; Indels 0; Gaps 0;

```

QY 3 AEEVVLQPIKEISGVKLPKSGKSLSNRIILLALAEITVVDNLNSEDVHYMLGALKTL 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 ASIVVQLPIRQISGLIKLPKSGKSLSNRIILLALAEITVVDNLNSEDVHYMLGALKTL 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 GLSVEADKAKRAVAVVCGCGKPFVEKDAKEVQLFLGNAGTAMRSITLAATAAGNATYV 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 GLNVERHSENNRAVVEGCGGIFPASIDSKSDIELYGNAGTAMRPLTAATAAGNATYV 191
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 LDGVPFMRERPIGDLVVGKQLGADVDCFLGDCPPVRVXGIGLPKGVKLSGSISSQY 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 LDGVPFMRERPIGDLVVGKQLGADVDCFLGDCPPVRVXGIGLPKGVKLSGSISSQY 251
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 LSAALMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVKAHSDSDMRFFVKGQKY 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 252 LTRALLMAAPLALGDVEIEITDKLISIPYEMTLRLMERFGVKAHSDSDMRFFVKGQKY 311
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 KSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLQGVKFAVLEMMGAKYTWTE 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 312 KSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTTSLQGVKFAVLEMMGAKYTWTE 371
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 TSVTVTGPOREPFGKRLKALIDVNMNMKPDVAMTLAVALFADGPTAIRDVASWRKYETE 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 372 NSVTYVGPBRDAFGMRLRAIDVNMNMKPDVAMTLAVALFADGPTAIRDVASWRKYETE 431
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 363 RMAVITELTKLGAASVEEGDLCITPPEKLANVTAIDTDDHMMMAFSLAACADVPVIT 422
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 432 RMAVITELTKLGAATVEEGSDYCVITPPKVPKPAEIDTDDHMMMAFSLAACADVPVIT 491
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 423 RDGCTRKTFPDYFDVLTSTFVN 445
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 492 KDGCTRKTFPDYFDVLEIRTKH 514
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 15

AR01 TOBAC STANDARD; PRT; 518 AA.
AC P23981;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase 1, chloroplast precursor
DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase 1) (EPSP
synthase 1).
GN Name=EPSPS-1;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92032779; PubMed=1932690;
Wang Y., Jones J., Weller S., Goldsbrough P. B.;
RT "Expression and stability of amplified genes encoding 5-
enolpyruvylshikimate-3-phosphate synthase in glycosylate-tolerant
tobacco cells.";
RL Plant Mol. Biol. 17:1127-1138 (1991).
CC -1- CATALYTIC ACTIVITY: phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBCELLULAR LOCATION: Chloroplast.

```
CC -1- MISCELLANEOUS: This enzyme is the target of the potent, broad-  
CC spectrum herbicide, glyphosate [n-(phosphonomethyl)glycine].  
CC Overproduction of EPSP leads to glyphosate tolerance.  
CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to license@1sb-sib.ch).  
CC -----  
DR EMBL; M61904; AAA34071.1; -  
DR PIR; S18353; S18353.  
DR HSSP; P07638; 1G6S.  
DR InterPro; IPR006264; AroA.  
DR InterPro; IPR001986; EPSP_synth.  
DR Pfam; PF00275; EPSP_synthase; 1.  
DR ProDom; PD001867; EPSP_synth; 1.  
DR TIGRFAMs; TIGR01356; aroA; 1.  
DR PROSITE; PS00104; EPSP_Synthase_1; 1.  
DR PROSITE; PS00885; EPSP_Synthase_2; 1.  
KW Aromatic amino acid biosynthesis; Chloroplast; Transferase;  
KW Aromatic peptide.  
KW TRANSIT 1 74 Chloroplast.  
FT TRANSIT 1 74 3-phosphoshikimate 1-  
FT CHAIN 75 518 carboxyvinyltransferase 1.  
FT FT 4F03C514EAFB1681 CRC64;  
SQ SEQUENCE 518 AA; 55711 MW; 4F03C514EAFB1681 CRC64;  
  
Query Match 84.0%; Score 1896; DB 1; Length 518;  
Best Local Similarity 82.8%; Pred. No. 6.2e-122;  
Matches 365; Conservative 37; Mismatches 39; Indels 0; Gaps 0;  
  
QY 5 EVVLQPIKEISGVVKKLPGSLSLSNRILLALAGTTVDNLNSEDVHYMLGALTKLGL 64  
DB 78 EIVLQPIKDISGVTKLPGSKSLNRILLALAGRTVDNLLSDDIHMYLGALTKLGL 137  
QY 65 SVEADKAKRAVAVVGGCGKFPVEKAKEVOLFAGNAGTAMRSLLTAAVTAAGNATYVLD 124  
DB 138 HVEDDNEHQRAIIVEGCGGQFPVGKSSSEELQFLGNAGTAMRPLTAAVTVAGHSRYLD 197  
QY 125 GVPFRMRERPIGDLVVGKQAGADVCEPLGTDCEPPVRVKIGLPGGKVKLSGSISQYLS 184  
DB 198 GVPFRMRERPIGDLVVGKQAGADVCEPLGTDCEPPVRIVSKGLPGGKVKLSGSISQYLT 257  
QY 185 ALLMAAPLALGDVEIEIIDLISIPYEMTLRLMERGVKAEHSDSWDRFYIKGGQKYKS 244  
DB 258 ALLMAAPLALGDVEIEIIDLISIPYEMTLRLMERGVKAEHSDSWDRFYIKGGQKYKS 317  
QY 245 PKNAVVEGDASSASYFLAGAITGGTAVTEGCGTSLQGDVVKFAEVLMMGAKVTWTETS 304  
DB 318 PKRAIYVGDASSASYFLAGAAVVGITVTEGCGTSLQGDVVKFAEVLMMGAEVWTENS 377  
QY 305 VTYTGQREPFGRKHLKAIDVNNMKMPDVAMTLAVVALPADGPTAIRDVASWRVKETERM 364  
DB 378 VTYVGPFRNSSGMKHLRAVDVNNMKMPDVAMTLAVVALPADGPTAIRDVASWRVKETERM 437  
QY 365 VAIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPYTIKD 424  
DB 438 IAICTELRKLGATVVEGSDYCIITPPEKLVNTAIDTYDDHRMAAFSLAACADVPYTIKD 497  
QY 425 PGCTRKTEPPDYFDVLSFVKN 445  
DB 498 PGCTRKTEPPDYFDVLSFVKN 518
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2005, 13:47:04 ; Search time 42 Seconds

(without alignment)
790.925 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256
Sequence: 1 AGAEEVVLQPIKISGVKL.....GCTRKTPPYFDVLTSTFVNK 445

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
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6: /cgn2_6/prodata/1/aa/6E_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2256	100.0	445	US-09-800-130A-7	Sequence 7, Appl1
2	2199.5	97.5	444	US-09-243-374-5	Sequence 5, Appl1
3	2199.5	97.5	444	US-09-000-062-3	Sequence 3, Appl1
4	2199.5	97.5	444	US-08-945-144A-3	Sequence 3, Appl1
5	2198.5	97.5	444	US-09-000-062-5	Sequence 5, Appl1
6	2198.5	97.5	444	US-08-945-144A-5	Sequence 5, Appl1
7	2196.5	97.4	570	US-08-832-078-5	Sequence 5, Appl1
8	2196.5	97.4	570	US-09-698-789B-5	Sequence 5, Appl1
9	2194.5	97.3	444	US-08-476-008-56	Sequence 5, Appl1
10	2194.5	97.3	444	US-08-306-063-56	Sequence 5, Appl1
11	2194.5	97.3	444	US-08-833-485-56	Sequence 5, Appl1
12	2194.5	97.3	444	US-09-137-440-56	Sequence 5, Appl1
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16	1927	85.4	444	US-08-306-063-55	Sequence 5, Appl1
17	1927	85.4	444	US-08-833-485-55	Sequence 5, Appl1
18	1927	85.4	444	US-09-243-374-1	Sequence 1, Appl1
19	1927	85.4	444	US-09-137-440-55	Sequence 5, Appl1
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21	1915	84.9	444	US-08-476-008-51	Sequence 5, Appl1
22	1911	84.7	444	US-08-476-008-51	Sequence 5, Appl1
23	1911	84.7	444	US-08-306-063-51	Sequence 5, Appl1
24	1911	84.7	444	US-08-833-485-51	Sequence 5, Appl1
25	1911	84.7	444	US-09-137-440-51	Sequence 5, Appl1
26	1901	84.3	444	US-09-243-374-3	Sequence 3, Appl1
27	1898	84.1	516	US-09-243-374-3	Sequence 3, Appl1

28	1898	84.1	516	6	5186642-4	Patent No. 5186642
29	1896	84.0	444	1	US-08-476-008-53	Sequence 53, Appl1
30	1896	84.0	444	1	US-08-306-063-53	Sequence 53, Appl1
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32	1896	84.0	444	3	US-09-137-440-53	Sequence 53, Appl1
33	1888	83.7	444	1	US-08-476-008-52	Sequence 52, Appl1
34	1888	83.7	444	1	US-08-306-063-52	Sequence 52, Appl1
35	1888	83.7	444	1	US-08-833-485-52	Sequence 52, Appl1
36	1888	83.7	444	3	US-09-137-440-52	Sequence 52, Appl1
37	1881.5	83.4	444	3	US-09-243-374-2	Sequence 4, Appl1
38	1880	83.3	444	3	US-08-476-008-54	Sequence 54, Appl1
39	1877	83.2	444	1	US-08-306-063-54	Sequence 54, Appl1
40	1877	83.2	444	1	US-08-833-485-54	Sequence 54, Appl1
41	1877	83.2	444	3	US-09-137-440-54	Sequence 54, Appl1
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43	1874	83.1	444	6	5310667-3	Patent No. 5310667
44	1874	83.1	444	6	5310667-3	Patent No. 5310667
45	1869.5	82.9	446	6	5310667-4	Patent No. 5310667

ALIGNMENTS

RESULT 1									
US-09-800-130A-7									
Sequence 7, Application US/09800130A									
Patent No. 6803501									
GENERAL INFORMATION:									
APPLICANT: Baerson, Scott									
APPLICANT: Heck, Gregory									
APPLICANT: Rodriguez, Damian									
TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions									
FILE REFERENCE: 60/188,093									
CURRENT FILING DATE: US/09/800,130A									
NUMBER OF SEQ ID NOS: 16									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 7									
LENGTH: 445									
TYPE: PRT									
ORGANISM: Eleusine indica									
US-09-800-130A-7									
Query Match									
Best Local Similarity 100.0%; Score 2256; DB 4; Length 445;									
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	121	YVLDGVPKREKRPIDGLVGLKQLGADVDCFTGTCPPRYVKGIGLPGKAYKLSGIS	180						
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DB	181	QYLSALMAAPALADGVEIITDKLISIPYVMTLRIMRFGVKAHSHSMDRPFYIKGQ	240						
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DB	241	KYKSPKNAVVEGDASASYFLAGAAITGGTIVVGGCTTSLQGDVYFAVLEEMGAKVTM	300						
QY	301	TETSVTVTPQEPFGRKRLKAIIDVNMGMPPVANTLAVVAFPAQPTAIRVVASRVKE	360						
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QY	361	TERMAVIRTELKRLGASVEGDYCIITPEKANTAJAITTYDDHNNAMAFSLAACADVAV	420						
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Db 361 TERMVAIRTELTKGASVEBGLDYCIITPEKLNVTAITDYDDHMAAFSLAACADVPV 420
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Db 421 TIRDPGCTRKTPPDYFDVLTSTFVN 445

RESULT 2

US-09-243-374-5
; Sequence 5; Application US/09243374B
; Patent No. 6225114
; GENERAL INFORMATION:
; APPLICANT: Eichholtz, David Alan
; APPLICANT: Gasser, Charles Scott
; APPLICANT: Kishore, Ganesh M
; TITLE OF INVENTION: Glycoester-tolerant 5-enolpyruvyl-3-phosphoshikimate
; TITLE OF INVENTION: synthases
; FILE REFERENCE: EESP synthases
; CURRENT APPLICATION NUMBER: US/09/243,374B
; EARLIER FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 07/590,647
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-09-243-374-5

Query Match 97.5%; Score 2199.5; DB 3; Length 444;
Best Local Similarity 97.5%; Pred. No. 1,7e-215;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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Db 61 TLGLSVEADKAKRAVAVVCGGKFPVE-DAKEEVOLFLGNAGTAMRPLTAATAAGGNAT 119
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Db 121 YVLGVPRMRERPIGDLVGLKQLGADVDFLGTDCPPRVVNGIGLPGKVKLSGSIS 179
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Db 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMERFGVKAHSDSWDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTISLOGDYKFAEVLMMGAKVTW 300
Db 241 KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTISLOGDYKFAEVLMMGAKVTW 299
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Db 301 TESTSVTVGPBREPRGRKHLKALIDVNMNKMPPVAMTLAVVALPADGPTAIRDVASRWYK 359
QY 361 TERMVAIRTELTKGASVEBGLDYCIITPEKLNVTAITDYDDHMAAFSLAACADVPV 420
Db 361 TERMVAIRTELTKGASVEBGLDYCIITPEKLNVTAITDYDDHMAAFSLAACADVPV 419
QY 421 TIRDPGCTRKTPPDYFDVLTSTFVN 445
Db 421 TIRDPGCTRKTPPDYFDVLTSTFVN 444

RESULT 3

US-09-000-062-3
; Sequence 3; Application US/09000062
; Patent No. 6338961
; GENERAL INFORMATION:
; APPLICANT: DEROSE, Richard

; APPLICANT: CHAUBERT, Nicole
; APPLICANT: GIGOT, Claude (deceased)
; TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
; TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
; FILE REFERENCE: 022650-453
; CURRENT APPLICATION NUMBER: US/09/000,062
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/FR96/01109
; EARLIER FILING DATE: 1996-07-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-09-000-062-3

Query Match 97.5%; Score 2199.5; DB 3; Length 444;
Best Local Similarity 97.5%; Pred. No. 1,7e-215;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

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Db 1 AGAEEVVLQPIKEISGVNKLPGSKLSNRILLLSALAEGETTVVDNLINSEVDHYMIGALK 60
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Db 61 TLGLSVEADKAKRAVAVVCGGKFPVE-DAKEEVOLFLGNAGTAMRPLTAATAAGGNAT 119
QY 121 YVLGVPRMRERPIGDLVGLKQLGADVDFLGTDCPPRVVNGIGLPGKVKLSGSIS 180
Db 121 YVLGVPRMRERPIGDLVGLKQLGADVDFLGTDCPPRVVNGIGLPGKVKLSGSIS 179
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Db 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRMERFGVKAHSDSWDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTISLOGDYKFAEVLMMGAKVTW 300
Db 241 KYKSPKNAVVEGDASASAYFLAGAAITGGTVVEGCGTISLOGDYKFAEVLMMGAKVTW 299
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Db 301 TESTSVTVGPBREPRGRKHLKALIDVNMNKMPPVAMTLAVVALPADGPTAIRDVASRWYK 359
QY 361 TERMVAIRTELTKGASVEBGLDYCIITPEKLNVTAITDYDDHMAAFSLAACADVPV 420
Db 361 TERMVAIRTELTKGASVEBGLDYCIITPEKLNVTAITDYDDHMAAFSLAACADVPV 419
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Db 421 TIRDPGCTRKTPPDYFDVLTSTFVN 444

RESULT 4

US-08-945-144A-3
; Sequence 3; Application US/08945144A
; Patent No. 6566587
; GENERAL INFORMATION:
; APPLICANT: Lebrun, Michel
; APPLICANT: Salland, Alain
; APPLICANT: Freysinet, Georges
; APPLICANT: Degryse, Eric
; TITLE OF INVENTION: Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
; TITLE OF INVENTION: Gene Coding for Said Protein and Transformed Plants
; FILE REFERENCE: 5500-13
; CURRENT APPLICATION NUMBER: US/08/945,144A
; EARLIER FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: PCT/FR96/01125


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/ PRIOR FILING DATE: 1996-07-18
/ PRIOR APPLICATION NUMBER: FRANCE 95/08979
/ PRIOR FILING DATE: 1995-07-19
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 444
/ TYPE: DRT
/ ORGANISM: Zea mays
US-08-945-144A-3

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Query Match	97.5%	Score 2199.5;	DB 4;	Length 444;
Best Local Similarity	97.5%;	Pred. No. 1.7e-215;		
Matches 434;	Conservative 5;	Mismatches 5;	Indels 1;	Gaps 1;

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Db	1	AGAEVILQCIKEISGVKLPGSKISJNSNILLLSALAEQTVVDNLNSEDVHYMLGK	60
Qy	61	TLGLSVADKAARAAVAVVGGCGKFPVEKDAKEEVOFLGNAGTAMRSITTAATAAGGNAT	120
Db	61	TLGLSVADKAARAAVAVVGGCGKFPVE-DAKEEVOFLGNAGTAMRPLTAATAAGGNAT	119
Qy	121	YVLDSVPRMERPIGDLVGLVKQLGADVDCFLCTCCPPRXYKGGIPGKVKISGSISS	188
Db	120	YVLDSVPRMERPIGDLVGLVKQLGADVDCFLCTCCPPRVNNGIGLPGKVKISGSISS	179
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Db	180	QYLSALLMAAPLALGDBVEIIDIKLISIPYEMTLRLMERFGVKAHSDSMDREYIKGGQ	239
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Db	300	TEFSVTYVTPGQEPFQRKHLKAIIDVMNMGHPVANTLAVALLPADGPALIIDVASMRYKE	358
Qy	361	TEEMVAIRTELTLGLASVEBGLDYCIITPBEKLNATAIDTYDDHRMAMAFSLAACADVPV	420
Db	360	TEEMVAIRTELTLGLASVEBGPDYCIITPBEKLNATAIDTYDDHRMAMAFSLAACAEVPV	419
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Db	420	TIRDPGCTRKTPEDVYEDULSTPKN	444

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RESULT 5
US-09-000-062-5
/ Sequence 5, Application US/09000062
/ Patent No. 6338961
/ GENERAL INFORMATION:
/ APPLICANT: DEROSE, Richard
/ APPLICANT: CHABERT, Nicole
/ APPLICANT: GIGOT, Claude (deceased)
/ TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
/ TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
/ TITLE OF INVENTION: TRANSFORMATION OF PLANTS
/ FILE REFERENCE: 022650-453
/ CURRENT APPLICATION NUMBER: US/09/000,062
/ CURRENT FILING DATE: 1998-05-29
/ EARLIER APPLICATION NUMBER: PCT/FR96/01109
/ EARLIER FILING DATE: 1996-07-17
/ EARLIER APPLICATION NUMBER: FR 95/08980
/ EARLIER FILING DATE: 1995-07-19
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Zea mays
/ US-09-000-062-5

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Query Match	97.5%	Score 2198.5;	DB 3;	Length 444;
Best Local Similarity	97.5%	Pred. No. 2.1e-215;		
Matches 434; Conservative	5;	Mismatches 5;	Indels 1;	Gaps 1

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Db	1	AGEEIVLQPIEIGSVGLPGSKLSISN	11L5LALAEGLTVVDNLNSEDHYMGLAK	60
QY	61	TLGLSEADKAAKRAVWVGCGGKFPVEKDAKEBVL	FLGNAGTAMSLTAATVAAGNAT	120
Db	61	TLGLSEADKAAKRAVWVGCGGKFPVE	DAKEBVLFLGNAGTAMSLTAATVAAGNAT	119
QY	121	YVLDSVPRMRERPIDDLVWGLKQLGADNDC	FLGTGCPFRVVGIGLPGGKYGLSSSIS	180
Db	120	YVLDSVPRMRERPIDDLVWGLKQLGADNDC	FLGTGCPFRVVGIGLPGGKYGLSSSIS	179
QY	181	QYLSALLMAAPALGDVEIEITDKLISIPYEMTL	RLMERFGVKAHSDSMDFYIKGGQ	240
Db	180	QYLSALLMAAPALGDVEIEITDKLISIPYEMTL	RLMERFGVKAHSDSMDFYIKGGQ	239
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Db	240	KKSPFPAIVYEBGDASSASYFLAGAALTG	TVTVBEGCITSLQGDVFAVYLEMMGAKVTW	299
QY	301	TETSLTVWGPQEBEPGRKHLKALIDVNMNM	MPVAMTLAAVALFADOPTAIRDVASRYKE	360
Db	300	TETSLTVWGPQEBEPGRKHLKALIDVNMNM	MPVAMTLAAVALFADOPTAIRDVASRYKE	359
QY	361	TERMAVIRTELTKLGASVEBGLDYCIITPE	PEKLTANTALIDTYDHRMAAFSLAACADVY	420
Db	360	TERMAVIRTELTKLGASVEBGLDYCIITPE	PEKLTANTALIDTYDHRMAAFSLAACADVY	419
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RESULT 6
US-08-945-144A-5
: Sequence 5, Application US/08945144A
: Patent No. 6566587
: GENERAL INFORMATION:
: APPLICANT: Ledrùn, Michel
: APPLICANT: Sailland, Alain
: APPLICANT: Freyssinet, Georges
: APPLICANT: Degryse, Eric
: TITLE OF INVENTION: Mutated 5'-End Pyruvylkinimate-3-Phosphate Synthase
: TITLE OF INVENTION: Gene Coding for Said Protein and Transformed Plants
: TITLE OF INVENTION: Containing Said Gene
: FILE REFERENCE: 5500-13
: CURRENT APPLICATION NUMBER: US/08/945,144A
: CURRENT FILING DATE: 1998-01-20
: PRIOR APPLICATION NUMBER: PCT/FR96/01125
: PRIOR FILING DATE: 1996-07-18
: PRIOR APPLICATION NUMBER: FRANCE 95/08979
: PRIOR FILING DATE: 1995-07-19
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 444
: TYPE: PRT
: ORGANISM: Zea mays
US-08-945-144A-5

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Query Match	97.5%	Score 2198.5	DB 4	Length 444
Best Local Similarity	97.5%	Pred. No. 2.1e-215		
Matches 434	Conservative 5	Mismatches 5	Indels 1	Gaps 1
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DB	1	AGAEELVQPIKKEISGVYKLPKGSKSLNRIILLNAALEGGTVVNDNLNSDEVHYMLGALK	60	

Qy 61 TLGLSEADKAKRAVAVVGGCGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 120
Db 61 TLGLSEADKAKRAVAVVGGCGKFPVE -DAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 119
Qy 121 YVLDDGVRMRERPIGDLVVGKLGADVDFLGTDCCPVAVKIGLPGSKVLSGSIS 180
Db 120 YVLDDGVRMRERPIGDLVVGKLGADVDFLGTDCCPVAVNGIGLPGSKVLSGSIS 179
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Db 180 QYLSALLMAAPLALGDVEIIRIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 239
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Db 240 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTSLQGDVKAFAVLEMMGAKVTM 299
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Db 360 TERMVAIIRTELTKLGASVEEGDYCIITPEKLTANTAITDYDDHRMAMAFSLAACADVPY 419
Qy 421 TIRDPGCTRKTPDPYFDVLSFVKN 445
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RESULT 7

US-08-832-078-5
/ Sequence 5, Application US/08832078
/ Patent No. 6040497
/ GENERAL INFORMATION:
/ APPLICANT: SPENCER, MICHAEL
/ APPLICANT: MUMM, RITA
/ APPLICANT: GWYN, JEFF
/ TITLE OF INVENTION: GLYPHOSATE RESISTANCE MAIZE LINES
/ FILE REFERENCE: DEKM:132
/ CURRENT APPLICATION NUMBER: US/08/832,078
/ CURRENT FILING DATE: 1997-04-03
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 570
/ TYPE: PRN
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Primer
US-08-832-078-5

Query Match 97.4%; Score 2196.5; DB 3; Length 570;
Best Local Similarity 97.3%; Pred. No. 5.1e-215;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
Qy 1 AGAEEVVLQPIKEISGVVKLPGSKLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 60
Db 127 AGAEEIVLQPIKEISGVVKLPGSKLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 186
Qy 61 TLGLSEADKAKRAVAVVGGCGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 120
Db 187 TLGLSEADKAKRAVAVVGGCGKFPVE -DAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 245
Qy 121 YVLDDGVRMRERPIGDLVVGKLGADVDFLGTDCCPVAVKIGLPGSKVLSGSIS 180
Db 246 YVLDDGVRMRERPIGDLVVGKLGADVDFLGTDCCPVAVNGIGLPGSKVLSGSIS 305
Qy 181 QYLSALLMAAPLALGDVEIIRIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Db 306 QYLSALLMAAPLALGDVEIIRIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 365
Qy 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTSLQGDVKAFAVLEMMGAKVTM 300

Db 366 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTSLQGDVKAFAVLEMMGAKVTM 425
Qy 301 TETSVTVTGPOREPFGKRLKALDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYKE 360
Db 426 TETSVTVTGPOREPFGKRLKALDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYKE 485
Qy 361 TERMVAIIRTELTKLGASVEEGDYCIITPEKLTANTAITDYDDHRMAMAFSLAACADVPY 420
Db 486 TERMVAIIRTELTKLGASVEEGDYCIITPEKLTANTAITDYDDHRMAMAFSLAACADVPY 545
Qy 421 TIRDPGCTRKTPDPYFDVLSFVKN 445
Db 546 TIRDPGCTRKTPDPYFDVLSFVKN 570

RESULT 8

US-09-698-789B-5
/ Sequence 5, Application US/09698789B
/ Patent No. 6762344
/ GENERAL INFORMATION:
/ APPLICANT: SPENCER, MICHAEL
/ APPLICANT: MUMM, RITA
/ APPLICANT: GWYN, J. JEFFERSON
/ APPLICANT: MCELROY, DAVID
/ APPLICANT: STEPHENS, MICHAEL A.
/ TITLE OF INVENTION: METHOD FOR PLANT BREEDING
/ FILE REFERENCE: DEKM:157USC1
/ CURRENT APPLICATION NUMBER: US/09/698,789B
/ CURRENT FILING DATE: 2000-10-07
/ PRIOR APPLICATION NUMBER: 08/927,368
/ PRIOR FILING DATE: 1997-09-11
/ PRIOR APPLICATION NUMBER: 08/899,247
/ PRIOR FILING DATE: 1997-07-23
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 570
/ TYPE: PRN
/ ORGANISM: Zea mays
US-09-698-789B-5

Query Match 97.4%; Score 2196.5; DB 4; Length 570;
Best Local Similarity 97.3%; Pred. No. 5.1e-215;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
Qy 1 AGAEEVVLQPIKEISGVVKLPGSKLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 60
Db 127 AGAEEIVLQPIKEISGVVKLPGSKLSNRILLLSALABGTTVVDNLNSEDVHYMLGALK 186
Qy 61 TLGLSEADKAKRAVAVVGGCGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 120
Db 187 TLGLSEADKAKRAVAVVGGCGKFPVE -DAKEEVOLFLGNAGTAMRSLTAATTAAGGNAT 245
Qy 121 YVLDDGVRMRERPIGDLVVGKLGADVDFLGTDCCPVAVKIGLPGSKVLSGSIS 180
Db 246 YVLDDGVRMRERPIGDLVVGKLGADVDFLGTDCCPVAVNGIGLPGSKVLSGSIS 305
Qy 181 QYLSALLMAAPLALGDVEIIRIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Db 306 QYLSALLMAAPLALGDVEIIRIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 365
Qy 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTSLQGDVKAFAVLEMMGAKVTM 300
Db 366 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTSLQGDVKAFAVLEMMGAKVTM 425
Qy 301 TETSVTVTGPOREPFGKRLKALDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYKE 360
Db 426 TETSVTVTGPOREPFGKRLKALDVNMNKMPPVANTLAVVALFADGPTAIRDVASRWYKE 485
Qy 361 TERMVAIIRTELTKLGASVEEGDYCIITPEKLTANTAITDYDDHRMAMAFSLAACADVPY 420
Db 486 TERMVAIIRTELTKLGASVEEGDYCIITPEKLTANTAITDYDDHRMAMAFSLAACADVPY 545

QY 421 TIRDPGCTRKTPDPYDVULSTFVKN 445
DB 546 TIRDPGCTRKTPDPYDVULSTFVKN 570

RESULT 9

US-08-476-008-56
Sequence 56, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-008-56

Query Match 97.3%; Score 2194.5; DB 1; Length 444;
Best Local Similarity 97.3%; Pred. No. 5.5e-215;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVVKLPGSKSLNRILLISALAEGLTVVVDNLINSEDAVYMLGALK 60
DB 1 AGAEEIVLQPIKISGVVVKLPGSKSLNRILLISALAEGLTVVVDNLINSEDAVYMLGALK 60
QY 61 TLGLSTVADAKAARAVVVGCGKFPVKKAKERYQLFLGAGTAMSLTAATTAAGNAT 120
DB 61 TLGLSTVADAKAARAVVVGCGKFPVKKAKERYQLFLGAGTAMSLTAATTAAGNAT 119
QY 121 YVLDGVPRMRERIPGDLVVLKQLGADVDFLGTDCPPVAVKIGLPGSKVTLSSGIS 180
DB 121 YVLDGVPRMRERIPGDLVVLKQLGADVDFLGTDCPPVAVKIGLPGSKVTLSSGIS 180

DB 120 YVLDGVPRMRERIPGDLVVLKQLGADVDFLGTDCPPVAVKIGLPGSKVTLSSGIS 179
QY 181 QYISALLMAAPLALGDVEIEIIDKLISIPVENTLILMERFGYKAHSDSMDRFYIKGGQ 240
DB 180 QYISALLMAAPLALGDVEIEIIDKLISIPVENTLILMERFGYKAHSDSMDRFYIKGGQ 239
QY 241 KYKSPKNAVVEGASASVFLAGAAITGGTAVYEGGCTTSLQDVKFAVLEMMGAKVM 300
DB 240 KYKSPKNAVVEGASASVFLAGAAITGGTAVYEGGCTTSLQDVKFAVLEMMGAKVM 299
QY 301 TETSVTVTGPOREPFRKHLKAIIDVNMNKPVDVAMTLAVVALPADGPTAIRDVAASRYKE 360
DB 300 TETSVTVTGPOREPFRKHLKAIIDVNMNKPVDVAMTLAVVALPADGPTAIRDVAASRYKE 359
QY 361 TERMAVIRTELTKGASVEBGDYCIITPEKLVNTAIDTYDDHRNMAFSLAACADV 420
DB 360 TERMAVIRTELTKGASVEBGDYCIITPEKLVNTAIDTYDDHRNMAFSLAACADV 419
QY 421 TIRDPGCTRKTPDPYDVULSTFVKN 445
DB 420 TIRDPGCTRKTPDPYDVULSTFVKN 444

RESULT 10

US-08-306-063-56
Sequence 56, Application US/08306063
Patent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6047
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-306-063-56

Query Match	97.3%	Score 2194.5;	DB 1;	Length 444;
Best Local Similarity	97.3%;	Pred. No. 5.5e-215;		
Matches 433; Conservative	5;	Mismatches 6;	Indels 1;	Gaps 1;

[illegible]

RESULT 11
 US-08-833-485-56
 Sequence 56, Application US/08833485
 Patent No. 5804425
 GENERAL INFORMATION:
 APPLICANT: Barry, Gerard F.
 APPLICANT: Kishore, Ganesh M.
 APPLICANT: Padgett, Stephen R.
 APPLICANT: Stalling, William C.
 TITLE OF INVENTION: Glycosate Tolerant
 TITLE OF INVENTION: 5-hydroxytryptamine-3-Phosphate Synthases
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B44F
 STREET: 700 Chesterfield Village Parkway
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,485
 FILING DATE: 07-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,063
 FILING DATE: 13-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,611
 FILING DATE: 28-AUG-1991

```

: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/576,537
: FILING DATE: 31-AUG-1990
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner Jr., Dennis R.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21 (15117)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)737-6099
: TELEFAX: (314)737-6047
: INFORMATION FOR SEQ ID NO: 56:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 444 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-853-485-56

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Query Match	97.3%;	Score 2194.5;	DB 1;	Length 444;
Best Local Similarity	97.3%;	Pred. No. 5.5e-215;		
Matches 433;	Conservative 5;	Mismatches 6;	Indels 1;	Gaps 1;

Qy	AGAEVVLQPIKEIGVYKLPOSSKLSNRILLLSALAEGLVDNLLNSDYHMYLGALE	60
Dd	1 AGAEVVLQPIKEIGVYKLPOSSKLSNRILLLSALAEGLVDNLLNSDYHMYLGALE	60
Qy	TIGLSVEADKAKRAVWVGCGGKPEVEKATEBVOFLGNAGTAMRSLTAAVTPAAGGNAT	120
Dd	61 TIGLSVEADKAKRAVWVGCGGKPEVE -DAKEBVOFLGNAGTAMRPLTAAVTPAAGGNAT	119
Qy	YVLDDGVRRRRERPIDGLVVGKQUGADVDCFLGNDCCPVYKIGSLPGKRVLSGSIS	180
Dd	121 YVLDDGVRRRRERPIDGLVVGKQUGADVDCFLGNDCCPVYKIGSLPGKRVLSGSIS	180
Qy	YVLDDGVRRRRERPIDGLVVGKQUGADVDCFLGNDCCPVYKIGSLPGKRVLSGSIS	179
Dd	120 YVLDDGVRRRRERPIDGLVVGKQUGADVDCFLGNDCCPVYKIGSLPGKRVLSGSIS	179
Qy	QYLSALMLMAAPALGDVEIEIILDKLISIPYEMTLRLMERFGVAEHSDSMDRPFYIKGQ	240
Dd	181 QYLSALMLMAAPALGDVEIEIILDKLISIPYEMTLRLMERFGVAEHSDSMDRPFYIKGQ	240
Qy	QYLSALMLMAAPALGDVEIEIILDKLISIPYEMTLRLMERFGVAEHSDSMDRPFYIKGQ	239
Dd	180 QYLSALMLMAAPALGDVEIEIILDKLISIPYEMTLRLMERFGVAEHSDSMDRPFYIKGQ	239
Qy	KYKSPKNAVVEGDASASYFLAGAAITGGTYVTEGCGTSLQGDYKFAVYLEMMGAKVTM	300
Dd	241 KYKSPKNAVVEGDASASYFLAGAAITGGTYVTEGCGTSLQGDYKFAVYLEMMGAKVTM	300
Qy	KYKSPKNAVVEGDASASYFLAGAAITGGTYVTEGCGTSLQGDYKFAVYLEMMGAKVTM	299
Dd	240 KYKSPKNAVVEGDASASYFLAGAAITGGTYVTEGCGTSLQGDYKFAVYLEMMGAKVTM	299
Qy	TERSVYVTPGOREPFGRRHKLKAIQVNMNMKMDVAMTLAAVALPADGTAIRDAVASRHYE	360
Dd	301 TERSVYVTPGOREPFGRRHKLKAIQVNMNMKMDVAMTLAAVALPADGTAIRDAVASRHYE	360
Qy	TERSVYVTPGOREPFGRRHKLKAIQVNMNMKMDVAMTLAAVALPADGTAIRDAVASRHYE	359
Dd	300 TERSVYVTPGOREPFGRRHKLKAIQVNMNMKMDVAMTLAAVALPADGTAIRDAVASRHYE	359
Qy	TERMAVARIETELTKLGASVEBGIDYCIITRPEKLNVTAIIDTYDDHRMAAFSLAACADVPY	420
Dd	361 TERMAVARIETELTKLGASVEBGIDYCIITRPEKLNVTAIIDTYDDHRMAAFSLAACADVPY	420
Qy	TERMAVARIETELTKLGASVEBGIDYCIITRPEKLNVTAIIDTYDDHRMAAFSLAACADVPY	419
Dd	360 TERMAVARIETELTKLGASVEBGIDYCIITRPEKLNVTAIIDTYDDHRMAAFSLAACADVPY	419
Qy	TIIRDPCCTKTPPYFDVLSITPVKN	445
Dd	421 TIIRDPCCTKTPPYFDVLSITPVKN	445
Qy	TIIRDPCCTKTPPYFDVLSITPVKN	444
Dd	420 TIIRDPCCTKTPPYFDVLSITPVKN	444

RESULT 12
US-09-137-440-56
Sequence 56, Application US/09137440
Patent No. 624876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stealing, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-holptryuylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: Dennis R. Hoerner, Jr., Monsanto Co. BBAP
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis

STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21 (15117) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEO ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-137-440-56

Query Match 97.3%; Score 2194.5; DB 3; Length 444;
Best Local Similarity 97.3%; Pred. No. 5.5e-215;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVLPKSGKSLNNRLLLSALAEGLTVVDNLNSBDVHYMGLAK 60
DB 1 AGAEEVVLQPIKISGVVLPKSGKSLNNRLLLSALAEGLTVVDNLNSBDVHYMGLAK 60
QY 61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 120
DB 61 TLGLSVADKAAKRAVAVVCGGKFPVE -DAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 119
QY 121 YVLGVPRRRERPIGDLVVLGKOLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 180
DB 120 YVLGVPRRRERPIGDLVVLGKOLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 179
QY 181 QVLSALMAAPLALGVEIEIIDKLSIPVENTLILMERFGVKAHSDSMRFFYIKGQ 240
DB 180 QVLSALMAAPLALGVEIEIIDKLSIPVENTLILMERFGVKAHSDSMRFFYIKGQ 239
QY 241 KYKSPNAAYVEGDASASYFLAGAAITGGTVVVEGCGTISLOGDVFAEVLMMGAKVTM 300
DB 240 KYKSPNAAYVEGDASASYFLAGAAITGGTVVVEGCGTISLOGDVFAEVLMMGAKVTM 299
QY 301 TETSVTVTGPQREPPFRKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVASVRVKE 360
DB 300 TETSVTVTGPQREPPFRKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVASVRVKE 359
QY 361 TERMAVIRTELTKLGSVSEGLDYCIITPEKLNVTALIDTYDDHMAAFSLAACAEVVP 420
DB 360 TERMAVIRTELTKLGSVSEGLDYCIITPEKLNVTALIDTYDDHMAAFSLAACAEVVP 419
QY 421 TIRDPCTRKTPDPDYDLSTFVN 445
DB 420 TIRDPCTRKTPDPDYDLSTFVN 444

RESULT 13
5310667-5
; Patent No. 5310667
; APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,
; GANESH M.
; TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL
; -3-PHOSPHOSHIKIMATE SYNTHASES
; NUMBER OF SEQUENCES: 37
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/380,963
; FILING DATE: 17-JUL-1989
; SEQ ID NO:5:
; LENGTH: 444
5310667-5

Query Match 96.7%; Score 2182.5; DB 6; Length 444;
Best Local Similarity 96.9%; Pred. No. 9.1e-214;
Matches 431; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKISGVVLPKSGKSLNNRLLLSALAEGLTVVDNLNSBDVHYMGLAK 60
DB 1 AGAEEVVLQPIKISGVVLPKSGKSLNNRLLLSALAEGLTVVDNLNSBDVHYMGLAK 60
QY 61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 120
DB 61 TLGLSVADKAAKRAVAVVCGGKFPVE -DAKEEVQLFLNAGTAMRSLTAAVTAAGNAT 119
QY 121 YVLGVPRRRERPIGDLVVLGKOLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 180
DB 120 YVLGVPRRRERPIGDLVVLGKOLGADVDCFLGTDCPPRVKGIIGLPGKVKLSGSISS 179
QY 181 QVLSALMAAPLALGVEIEIIDKLSIPVENTLILMERFGVKAHSDSMRFFYIKGQ 240
DB 180 QVLSALMAAPLALGVEIEIIDKLSIPVENTLILMERFGVKAHSDSMRFFYIKGQ 239
QY 241 KYKSPNAAYVEGDASASYFLAGAAITGGTVVVEGCGTISLOGDVFAEVLMMGAKVTM 300
DB 240 KYKSPNAAYVEGDASASYFLAGAAITGGTVVVEGCGTISLOGDVFAEVLMMGAKVTM 299
QY 301 TETSVTVTGPQREPPFRKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVASVRVKE 360
DB 300 TETSVTVTGPQREPPFRKHLKALDVNMNKMPPVAMTLAVVALPADGPTAIRVASVRVKE 359
QY 361 TERMAVIRTELTKLGSVSEGLDYCIITPEKLNVTALIDTYDDHMAAFSLAACAEVVP 420
DB 360 TERMAVIRTELTKLGSVSEGLDYCIITPEKLNVTALIDTYDDHMAAFSLAACAEVVP 419
QY 421 TIRDPCTRKTPDPDYDLSTFVN 445
DB 420 TIRDPCTRKTPDPDYDLSTFVN 444

RESULT 14
5310667-5
; Patent No. 5310667
; APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,
; GANESH M.
; TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL
; -3-PHOSPHOSHIKIMATE SYNTHASES
; NUMBER OF SEQUENCES: 37
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/380,963
; FILING DATE: 17-JUL-1989
; SEQ ID NO:5:
; LENGTH: 444
5310667-5

Query Match 96.7%; Score 2182.5; DB 6; Length 444;
Best Local Similarity 96.9%; Pred. No. 9.1e-214;
Matches 431; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

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QY      1 AGAEEVVLQPIKEISGVVLPKSGKSLSNRIILLALAEGLTVVDNLNSDEVHYMLGALK 60
      1 AGAEEVVLQPIKEISGVVLPKSGKSLSNRIILLALAEGLTVVDNLNSDEVHYMLGALK 60
DB      61 TLGLSVADKAAKRAVAVVGGCGKFPVEKDAKEEVQFLGNAGTAMRSLTAAVTAAGGNAT 120
      61 TLGLSVADKAAKRAVAVVGGCGKFPVE -DAKEEVQFLGNAGTAMRPLTAAVTAAGGNAT 119
QY      121 YVLDGVPKRRERIGDLVVGKQLGADVDCFLGTDGCPVAVNGIGLPGKVKLSGSISS 179
      120 YVLDGVPKRRERIGDLVVGKQLGADVDCFLGTDGCPVAVNGIGLPGKVKLSGSISS 179
QY      181 QYLSALMAAPLALGVEIEIIDLKLSIPYVENTLMLERFGVKAHSDSWDRFYIKGGQ 240
      180 QYLSALMAAPLALGVEIEIIDLKLSIPYVENTLMLERFGVKAHSDSWDRFYIKGGQ 239
DB      241 KYKSPKAAVVEGDASSASYFLAGAAITGGTVYEGCGTISLQGDVFAEYLEMGMKAKVTM 300
      240 KYKSPKAAVVEGDASSASYFLAGAAITGGTVYEGCGTISLQGDVFAEYLEMGMKAKVTM 299
QY      301 TETSUVTGPOREPFGRKHLKAIIDVMNMKMPDVAMTLAVVALFADGPTAIRDVASRWKYE 360
      300 TETSUVTGPOREPFGRKHLKAIIDVMNMKMPDVAMTLAVVALFADGPTAIRDVASRWKYE 359
DB      361 TERMAVIRTELTKLGASVEEGLDYCIITPPEKLNVTATIDYDDHRMAAFSLAACADVPY 420
      360 TERMAVIRTELTKLGASVEEGDPYCIITPPEKLNVTATIDYDDHRMAAFSLAACAEVY 419
QY      421 TIRDPGCTRKTPPDYFDVLTSTPVKN 445
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RESULT 15

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US-08-476-008-55
; Sequence 55, Application US/08476008
; Patent No. 5627061
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen M.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glycoside Tolerant
; TITLE OF INVENTION: 5-Ethoxyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,008
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.

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; REGISTRATION NUMBER: 30, 914
; REFERENCE/DOCKET NUMBER: 38-21(10660)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6099
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-008-55

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Query Match      85.4%; Score 1927; DB 1; Length 444;
Best Local Similarity 84.4%; Pred No. 1,1e-187;
Matches 312; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

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DB      65 SVADKAAKRAVAVVGGCGKFPVEKDAKEEVQFLGNAGTAMRSLTAAVTAAGGNATYVD 124
      64 HVEEDSANQRAVAVVGGCGGLFPVGKESKEIQLFLGNAGTAMRPLTAAVTAAGNSRYVD 123
QY      125 GVPKRRERIGDLVVGKQLGADVDCFLGTDGCPVAVNGIGLPGKVKLSGSISSOYLS 184
      124 GVPKRRERIGDLVVGKQLGADVDCFLGTDGCPVAVNGIGLPGKVKLSGSISSOYLT 183
DB      185 ALLMAAPLALGVEIEIIDLKLSIPYVENTLMLERFGVKAHSDSWDRFYIKGGQKYS 244
      184 ALLMAAPLALGVEIEIIDLKLSIPYVENTLMLERFGVKAHSDSWDRFYIKGGQKYS 243
QY      245 PKAAVVEGDASSASYFLAGAAITGGTVYEGCGTISLQGDVFAEYLEMGMKAKVTWTER 304
      244 PKAAVVEGDASSASYFLAGAAITGGTVYEGCGTISLQGDVFAEYLEMGMKAEVWTENS 303
DB      305 VTVTGPORPEPFGRKHLKAIIDVMNMKMPDVAMTLAVVALFADGPTAIRDVASRWKETER 364
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QY      365 VAIRTELTKLGASVEEGLDYCIITPPEKLNVTATIDYDDHRMAAFSLAACADVPVPTIR 424
      364 VAIRTELTKLGASVEEGDPYCIITPPEKLNVTATIDYDDHRMAAFSLAACADVPVPTI 423
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Search completed: September 15, 2005, 13:57:08
Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 13:55:40 ; Search time 185 Seconds
(without alignments)
974.015 Million cell updates/sec

Title: US-10-803-156-7

Perfect score: 2256

Sequence: 1 AGAEEVVLQPIKEISGVVL.....GCTRKTPPYFDVLSFVN 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	445	10 US-09-800-130A-7	Sequence 7, Appl1
2	2256	100.0	445	14 US-10-413-909-7	Sequence 7, Appl1
3	2256	100.0	445	18 US-10-803-156-7	Sequence 7, Appl1
4	2199.5	97.5	444	14 US-10-023-833-3	Sequence 3, Appl1
5	2199.5	97.5	444	14 US-10-214-766-22	Sequence 22, Appl1
6	2199.5	97.5	444	20 US-11-051-955-28	Sequence 28, Appl1
7	2198.5	97.5	444	14 US-10-023-833-5	Sequence 3, Appl1
8	2196.5	97.4	570	17 US-10-869-324-5	Sequence 5, Appl1
9	2194.5	97.3	444	9 US-09-861-696-56	Sequence 56, Appl1
10	2194.5	97.3	444	9 US-09-464-099A-56	Sequence 56, Appl1

12	2165	96.0	515	16 US-10-437-963-162988	Sequence 162988, Appl1
13	1929	85.5	391	14 US-10-214-766-20	Sequence 20, Appl1
14	1927	85.4	444	9 US-09-861-696-55	Sequence 55, Appl1
15	1927	85.4	444	9 US-09-464-099A-55	Sequence 55, Appl1
16	1927	85.4	516	14 US-10-214-766-24	Sequence 24, Appl1
17	1927	85.4	516	20 US-11-051-955-27	Sequence 27, Appl1
18	1918	85.0	444	10 US-09-791-489-9	Sequence 9, Appl1
19	1911	84.7	516	9 US-09-861-696-51	Sequence 51, Appl1
20	1911	84.7	444	9 US-09-464-099A-51	Sequence 51, Appl1
21	1911	84.7	516	14 US-10-214-766-28	Sequence 28, Appl1
22	1911	84.7	516	20 US-11-051-955-26	Sequence 26, Appl1
23	1898	84.1	534	15 US-10-424-599-194746	Sequence 194746, Appl1
24	1897	84.1	521	14 US-10-214-766-26	Sequence 26, Appl1
25	1896	84.0	444	9 US-09-861-696-53	Sequence 53, Appl1
26	1896	84.0	444	9 US-09-464-099A-53	Sequence 53, Appl1
27	1888	83.7	444	9 US-09-861-696-52	Sequence 52, Appl1
28	1888	83.7	444	9 US-09-464-099A-52	Sequence 52, Appl1
29	1888	83.7	520	14 US-10-214-766-27	Sequence 27, Appl1
30	1888	83.7	520	20 US-11-051-955-2	Sequence 2, Appl1
31	1877	83.2	444	9 US-09-861-696-54	Sequence 54, Appl1
32	1877	83.2	444	9 US-09-464-099A-54	Sequence 54, Appl1
33	1877	83.2	520	14 US-10-214-766-25	Sequence 25, Appl1
34	1664	73.8	347	14 US-10-214-766-21	Sequence 21, Appl1
35	1490	66.0	338	14 US-10-214-766-23	Sequence 23, Appl1
36	1264	56.0	248	15 US-10-425-114-43334	Sequence 43334, Appl1
37	1185	49.6	424	14 US-10-214-766-45	Sequence 45, Appl1
38	1116	49.5	426	14 US-10-214-766-43	Sequence 43, Appl1
39	1113.5	49.4	427	9 US-09-861-696-59	Sequence 59, Appl1
40	1113.5	49.4	427	9 US-09-464-099A-59	Sequence 59, Appl1
41	1113.5	49.4	427	14 US-10-214-766-46	Sequence 46, Appl1
42	1109.5	49.2	427	15 US-10-369-493-783	Sequence 783, Appl1
43	1108	49.1	427	9 US-09-861-696-60	Sequence 60, Appl1
44	1108	49.1	427	9 US-09-464-099A-60	Sequence 60, Appl1
45	1108	49.1	427	14 US-10-214-766-44	Sequence 44, Appl1

ALIGNMENTS

RESULT 1
US-09-800-130A-7
; Sequence 7, Appl1 Application US/09800130A
; Publication No. US20030188346A1
; GENERAL INFORMATION:
; APPLICANT: Baerleon, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damlan
; TITLE OF INVENTION: Method for Making Plants Tolerant to Glyphosate and Compositions
; FILE REFERENCE: 60/188,093
; CURRENT APPLICATION NUMBER: US/09/800,130A
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Eleusine indica
US-09-800-130A-7

Query Match	100.0%	Score 2256	DB 10	Length 445
Best Local Similarity	100.0%	Pred. No. 3.8e-199		
Matches 445	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	AGAEEVVLQPIKEISGVVLPGSKLSNRILLLSALAEETVVDMLNSEDVHMLGALK	60	
DB	1	AGAEEVVLQPIKEISGVVLPGSKLSNRILLLSALAEETVVDMLNSEDVHMLGALK	60	
QY	61	TIGLSVEADKAKRAVVGCCGKPFVEKDAKEEVQLFLGNACTAKRSLSLAATYAGGANT	120	
DB	61	TIGLSVEADKAKRAVVGCCGKPFVEKDAKEEVQLFLGNACTAKRSLSLAATYAGGANT	120	
QY	121	YTLGVPRRREPRIGDLVGLKOLGADVDCFLGTGCPPRVKGIGGLPGCKYKLSGSIS	180	

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Db      121  YVLDGVPNRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVKIGGLPGSKVYLSGSIS 180
Qy      181  QYLSALMLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKASHSDSMRFFYIKGQ 240
Db      181  QYLSALMLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKASHSDSMRFFYIKGQ 240
Qy      241  KYKSPKNAAYVEGDSSASYSYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
Db      241  KYKSPKNAAYVEGDSSASYSYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
Qy      301  TETSVTVTGPOREPFGKRLKALIDVNMNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
Db      301  TETSVTVTGPOREPFGKRLKALIDVNMNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
Qy      361  TERMVAIRTELTKLGASVEBGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db      361  TERMVAIRTELTKLGASVEBGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Qy      421  TIRDPGCTRKTPPDYFDVLSFVK 445
Db      421  TIRDPGCTRKTPPDYFDVLSFVK 445

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RESULT 2
US-10-413-909-7
; Sequence 7, Application US/10413909
; Publication No. US20030192072A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 11898.0019.00DVUS01 (MOBS019--1)
; CURRENT APPLICATION NUMBER: US/10/413,909
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/188,093
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Eleusine indica
US-10-413-909-7

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Query Match      100.0%; Score 2256; DB 14; Length 445;
Best Local Similarity 100.0%; Pred. No. 3,8e-199;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AGAEEVVLQPIKEISGVVVKLPGSKSLSNRIILLSALABGTTVDNLNSEDVHYMLGALK 60
Db      1  AGAEEVVLQPIKEISGVVVKLPGSKSLSNRIILLSALABGTTVDNLNSEDVHYMLGALK 60
Qy      61  TLGLSVEADKAKRAVAVVGGCGKFPVEKDACEVQVFLGNAGTARSLTAATTAAGNAT 120
Db      61  TLGLSVEADKAKRAVAVVGGCGKFPVEKDACEVQVFLGNAGTARSLTAATTAAGNAT 120
Qy      121  YVLDGVPNRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVKIGGLPGSKVYLSGSIS 180
Db      121  YVLDGVPNRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVKIGGLPGSKVYLSGSIS 180
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Db      181  QYLSALMLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKASHSDSMRFFYIKGQ 240
Qy      241  KYKSPKNAAYVEGDSSASYSYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
Db      241  KYKSPKNAAYVEGDSSASYSYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
Qy      301  TETSVTVTGPOREPFGKRLKALIDVNMNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
Db      301  TETSVTVTGPOREPFGKRLKALIDVNMNMPDVAMTLAVVALPADGPTAIRDVASWRVKE 360
Qy      421  TIRDPGCTRKTPPDYFDVLSFVK 445
Db      421  TIRDPGCTRKTPPDYFDVLSFVK 445

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Qy      361  TERMVAIRTELTKLGASVEBGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db      361  TERMVAIRTELTKLGASVEBGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
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Db      421  TIRDPGCTRKTPPDYFDVLSFVK 445

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RESULT 3
US-10-803-156-7
; Sequence 7, Application US/10803156
; Publication No. US20040148650A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 11898.0019.00DVUS02 (MOBS019--2)
; CURRENT APPLICATION NUMBER: US/10/803,156
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 60/188,093
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 09/800,130
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Eleusine indica
US-10-803-156-7

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Query Match      100.0%; Score 2256; DB 18; Length 445;
Best Local Similarity 100.0%; Pred. No. 3,8e-199;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  AGAEEVVLQPIKEISGVVVKLPGSKSLSNRIILLSALABGTTVDNLNSEDVHYMLGALK 60
Qy      61  TLGLSVEADKAKRAVAVVGGCGKFPVEKDACEVQVFLGNAGTARSLTAATTAAGNAT 120
Db      61  TLGLSVEADKAKRAVAVVGGCGKFPVEKDACEVQVFLGNAGTARSLTAATTAAGNAT 120
Qy      121  YVLDGVPNRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVKIGGLPGSKVYLSGSIS 180
Db      121  YVLDGVPNRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVKIGGLPGSKVYLSGSIS 180
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Db      181  QYLSALMLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKASHSDSMRFFYIKGQ 240
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Db      241  KYKSPKNAAYVEGDSSASYSYFLAGAAITGGTVVEGCGTISLOGDVKFAVLEMMGAKVTM 300
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Qy      361  TERMVAIRTELTKLGASVEBGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
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RESULT 4


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US-10-023-839-3
; Sequence 3, Application US/10023839
; Publication No. US20030027312A1
; GENERAL INFORMATION:
; APPLICANT: DEROSE, Richard
; APPLICANT: CHAUBERT, Nicole
; APPLICANT: GIGOT, Claude (deceased)
; TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
; TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
; TITLE OF INVENTION: TRANSFORMATION OF PLANTS
; FILE REFERENCE: 022650-453
; CURRENT APPLICATION NUMBER: US/10/023,839
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/000,062
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 95/08980
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-10-023-839-3

Query Match      97.5%; Score 2199.5; DB 14; Length 444;
Best Local Similarity 97.5%; Pred. No. 6.3e-194;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY      1 AGAEEVLPPIKEISGVVVLPGSKSLSNRIILLSALAEGETTVVDNLINSEVDHYMLGALK 60
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DB      1 AGAEEVLPPIKEISGVVVLPGSKSLSNRIILLSALAEGETTVVDNLINSEVDHYMLGALK 60
QY      61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGNAT 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 TLGLSVADKAAKRAVAVVCGGKFPVE-DAKEEVOLFLGNAGTAMRPLTAATTAAGNAT 119
QY      121 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      120 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISS 179
QY      181 QYLSALLMAAPLALGDVEIEIIDKLSIPYVEMTLRLMERFGVKAHSDSMRPFYIKGQ 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      180 QYLSALLMAAPLALGDVEIEIIDKLSIPYVEMTLRLMERFGVKAHSDSMRPFYIKGQ 239
QY      241 KXSPKNAAYVEGDASSASYFLAGAAITGGTVVVEGGGTTSLQGDVYKFAVLEMMGAKVTM 300
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QY      301 TETSVTVTGPOREPFGKRLKALIDVNMNMCPDVANTLAVVALPADGPTAIRDVASWRVKE 360
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      300 TETSVTVTGPOREPFGKRLKALIDVNMNMCPDVANTLAVVALPADGPTAIRDVASWRVKE 359
QY      361 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVAV 420
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      360 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVAV 419
QY      421 TIRDPGCTRKTPFDYDVLSTFVK 445
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DB      420 TIRDPGCTRKTPFDYDVLSTFVK 444

RESULT 5
US-10-214-766-22
; Sequence 22, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
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; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-10-214-766-22

Query Match      97.5%; Score 2199.5; DB 14; Length 444;
Best Local Similarity 97.5%; Pred. No. 6.3e-194;
Matches 434; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY      1 AGAEEVLPPIKEISGVVVLPGSKSLSNRIILLSALAEGETTVVDNLINSEVDHYMLGALK 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 AGAEEVLPPIKEISGVVVLPGSKSLSNRIILLSALAEGETTVVDNLINSEVDHYMLGALK 60
QY      61 TLGLSVADKAAKRAVAVVCGGKFPVEKDAKEEVOLFLGNAGTAMRSLTAATTAAGNAT 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 TLGLSVADKAAKRAVAVVCGGKFPVE-DAKEEVOLFLGNAGTAMRPLTAATTAAGNAT 119
QY      121 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      120 YVLDGVPKRRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISS 179
QY      181 QYLSALLMAAPLALGDVEIEIIDKLSIPYVEMTLRLMERFGVKAHSDSMRPFYIKGQ 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      180 QYLSALLMAAPLALGDVEIEIIDKLSIPYVEMTLRLMERFGVKAHSDSMRPFYIKGQ 239
QY      241 KXSPKNAAYVEGDASSASYFLAGAAITGGTVVVEGGGTTSLQGDVYKFAVLEMMGAKVTM 300
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      240 KXSPKNAAYVEGDASSASYFLAGAAITGGTVVVEGGGTTSLQGDVYKFAVLEMMGAKVTM 299
QY      301 TETSVTVTGPOREPFGKRLKALIDVNMNMCPDVANTLAVVALPADGPTAIRDVASWRVKE 360
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      300 TETSVTVTGPOREPFGKRLKALIDVNMNMCPDVANTLAVVALPADGPTAIRDVASWRVKE 359
QY      361 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVAV 420
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      360 TERMAAIRTELTKLGASVEEGDLYCIITPPEKLTNTAIDTYDDHRMAAFSLAACADVAV 419
QY      421 TIRDPGCTRKTPFDYDVLSTFVK 445
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      420 TIRDPGCTRKTPFDYDVLSTFVK 444

RESULT 6
US-11-051-955-28
; Sequence 28, Application US/11051955
; Publication No. US20050177899A1
; GENERAL INFORMATION:
; APPLICANT: Beetham, P.
; APPLICANT: Alesar, P.
; APPLICANT: Walker, K.
; APPLICANT: Metz, R.
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: 7991-086
; CURRENT APPLICATION NUMBER: US/11/051,955
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/09/685,403
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,027
; PRIOR FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 60/173,564
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-11-051-955-28
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Query Match 97.5%; Score 2199.5; DB 20; Length 444;
Best Local Similarity 97.5%; Pred. No. 6.3e-194;
Matches 444; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEAGTTVDNLINSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEAGTTVDNLINSEDVHYMLGALK 60
QY 61 TLGLSVEADKAKARAVVVGCGKFPVEKDAKEEVOLFLGNAGTAMRSLLTAATAAGNAT 120
DB 61 TLGLSVEADKAKARAVVVGCGKFPVE-DAKEEVOLFLGNAGTAMRPLTAATAAGNAT 119
QY 121 YVLGVPPMRERPIDGLVWGLKQLGADVDFLGTDCCPVRVYKIGGLPGKVKYLSGSIS 180
DB 120 YVLGVPPMRERPIDGLVWGLKQLGADVDFLGTDCCPVRVYKIGGLPGKVKYLSGSIS 179
QY 181 QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKASHSDSWDRFYIKGQ 240
DB 180 QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKASHSDSWDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTISLOGDYKFAVLEMMGAKVTM 300
DB 240 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTISLOGDYKFAVLEMMGAKVTM 299
QY 301 TESTSVTVGPBEPFGRKHLKALDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASRVKE 360
DB 300 TESTSVTVGPBEPFGRKHLKALDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASRVKE 359
QY 361 TERMAVAIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPY 420
DB 360 TERMAVAIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPY 419
QY 421 TIRDPGCTRKTPPDYFDVLTSTFVK 445
DB 420 TIRDPGCTRKTPPDYFDVLTSTFVK 444

RESULT 7
US-10-023-839-5
Sequence 5, Application US/10023839
Publication No. US20030027312A1
GENERAL INFORMATION:
APPLICANT: DEROSER, Richard
APPLICANT: CHAUBERT, Nicole
APPLICANT: GIGOT, Claude (deceased)
TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
TITLE OF INVENTION: ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
TITLE OF INVENTION: TRANSFORMATION OF PLANTS
FILE REFERENCE: 022650-453
CURRENT APPLICATION NUMBER: US/10/023,839
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/000,062
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 95/08980
PRIOR FILING DATE: EARLIER FILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 444
TYPE: PRT
ORGANISM: Zea mays
US-10-023-839-5

Query Match 97.5%; Score 2198.5; DB 14; Length 444;
Best Local Similarity 97.5%; Pred. No. 7.8e-194;
Matches 444; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEAGTTVDNLINSEDVHYMLGALK 60
DB 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEAGTTVDNLINSEDVHYMLGALK 60
QY 61 TLGLSVEADKAKARAVVVGCGKFPVEKDAKEEVOLFLGNAGTAMRSLLTAATAAGNAT 120
DB 61 TLGLSVEADKAKARAVVVGCGKFPVEKDAKEEVOLFLGNAGTAMRSLLTAATAAGNAT 120

DB 61 TLGLSVEADKAKARAVVVGCGKFPVE-DAKEEVOLFLGNAGTAMRSLLTAATAAGNAT 119
QY 121 YVLGVPPMRERPIDGLVWGLKQLGADVDFLGTDCCPVRVYKIGGLPGKVKYLSGSIS 180
DB 120 YVLGVPPMRERPIDGLVWGLKQLGADVDFLGTDCCPVRVYKIGGLPGKVKYLSGSIS 179
QY 181 QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKASHSDSWDRFYIKGQ 240
DB 180 QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKASHSDSWDRFYIKGQ 239
QY 241 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTISLOGDYKFAVLEMMGAKVTM 300
DB 240 KYKSPKNAVVEGDASSASYFLAGAAITGGTVVEGCGTISLOGDYKFAVLEMMGAKVTM 299
QY 301 TESTSVTVGPBEPFGRKHLKALDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASRVKE 360
DB 300 TESTSVTVGPBEPFGRKHLKALDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASRVKE 359
QY 361 TERMAVAIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPY 420
DB 360 TERMAVAIRTELTKLGASVEBGIDYCIITPPEKLVNTAIDTYDHRMAMAFSLAACADVPY 419
QY 421 TIRDPGCTRKTPPDYFDVLTSTFVK 445
DB 420 TIRDPGCTRKTPPDYFDVLTSTFVK 444

RESULT 8
US-10-869-324-5
Sequence 5, Application US/10869324
Publication No. US20050086719A1
GENERAL INFORMATION:
APPLICANT: SPENCER, MICHAEL
APPLICANT: MUMF, RITA
APPLICANT: GWYN, J. JEFFERSON
APPLICANT: MCELROY, DAVID
APPLICANT: STEPHENS, MICHAEL A.
TITLE OF INVENTION: METHOD FOR PLANT BREEDING
FILE REFERENCE: DEKM:157USC2
CURRENT APPLICATION NUMBER: US/10/869,324
CURRENT FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 09/698,789
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 08/927,368
PRIOR FILING DATE: 1997-09-11
PRIOR APPLICATION NUMBER: 08/899,247
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 570
TYPE: PRT
ORGANISM: Zea mays
US-10-869-324-5

Query Match 97.4%; Score 2196.5; DB 17; Length 570;
Best Local Similarity 97.3%; Pred. No. 1.7e-193;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEAGTTVDNLINSEDVHYMLGALK 60
DB 127 AGAEEVVLQPIKEISGVVYKLPKSKLSNRILLLSALAEAGTTVDNLINSEDVHYMLGALK 186
QY 61 TLGLSVEADKAKARAVVVGCGKFPVEKDAKEEVOLFLGNAGTAMRSLLTAATAAGNAT 120
DB 61 TLGLSVEADKAKARAVVVGCGKFPVE-DAKEEVOLFLGNAGTAMRSLTAATAAGNAT 245
QY 121 YVLGVPPMRERPIDGLVWGLKQLGADVDFLGTDCCPVRVYKIGGLPGKVKYLSGSIS 180
DB 120 YVLGVPPMRERPIDGLVWGLKQLGADVDFLGTDCCPVRVYKIGGLPGKVKYLSGSIS 305
QY 181 QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKASHSDSWDRFYIKGQ 240
DB 180 QYLSALIMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFVKASHSDSWDRFYIKGQ 240

Db 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 365
QY 241 KXSPKNAAYVEGDASSASYFLAGAAITGGTVYVEGCGTTSLOGDVYKAEVLEMMGAKVTW 300
Db 366 KXSPKNAAYVEGDASSASYFLAGAAITGGTVYVEGCGTTSLOGDVYKAEVLEMMGAKVTW 425
QY 301 TETSVTVTGPOREPFGKHLKALIDVNMNMKMPDVAMTLAVVALLFADGPTAIRDVASRWYKE 360
Db 426 TETSVTVTGPOREPFGKHLKALIDVNMNMKMPDVAMTLAVVALLFADGPTAIRDVASRWYKE 485
QY 361 TERMAVIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db 486 TERMAVIRTELTKLGASVEEGDPYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 545
QY 421 TIRDPCTRKTFPDYDVLSTFVK 445
Db 546 TIRDPCTRKTFPDYDVLSTFVK 570

RESULT 9

US-11-050-645-5
Sequence 5, Application US/11050645
Publication No. US2005018843A1
GENERAL INFORMATION:
APPLICANT: SPENCER, MICHAEL
APPLICANT: MUMM, RITA
APPLICANT: GWYN, J. JERPERSON
APPLICANT: MCELROY, DAVID
APPLICANT: STEPHENS, MICHAEL A.
TITLE OF INVENTION: METHOD FOR PLANT BREEDING
FILE REFERENCE: DEKM:157USC2
CURRENT APPLICATION NUMBER: US/11/050,645
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION NUMBER: US/10/869,324
PRIOR FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 09/698,789
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 08/927,368
PRIOR FILING DATE: 1997-09-11
PRIOR APPLICATION NUMBER: 08/899,247
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 570
TYPE: PRT
ORGANISM: Zea mays
US-11-050-645-5

Query Match 97.4%; Score 2196.5; DB 20; Length 570;
Best Local Similarity 97.3%; Pred. No. 1.7e-193;
Matches 433; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
QY 1 AGAEEVVLQPIKEISGVVVKLPGSKSLSNRILLLSALAEGLTVVDNLNLSSEVDHYMGLAK 60
Db 127 AGAEEVVLQPIKEISGVVVKLPGSKSLSNRILLLSALAEGLTVVDNLNLSSEVDHYMGLAK 186
QY 61 TLGLSEADKAAKRAVAVVCGGKFPVEKDAKEEVQLFLGNAGTAMRSLLTAATTAAGNAT 120
Db 187 TLGLSEADKAAKRAVAVVCGGKFPVE-DAKEEVQLFLGNAGTAMRSLLTAATTAAGNAT 245
QY 121 YVLGVPRMRERPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 180
Db 246 YVLGVPRMRERPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 305
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 240
Db 306 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 365
QY 241 KXSPKNAAYVEGDASSASYFLAGAAITGGTVYVEGCGTTSLOGDVYKAEVLEMMGAKVTW 300
Db 366 KXSPKNAAYVEGDASSASYFLAGAAITGGTVYVEGCGTTSLOGDVYKAEVLEMMGAKVTW 425

QY 301 TETSVTVTGPOREPFGKHLKALIDVNMNMKMPDVAMTLAVVALLFADGPTAIRDVASRWYKE 360
Db 426 TETSVTVTGPOREPFGKHLKALIDVNMNMKMPDVAMTLAVVALLFADGPTAIRDVASRWYKE 485
QY 361 TERMAVIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420
Db 486 TERMAVIRTELTKLGASVEEGDPYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 545
QY 421 TIRDPCTRKTFPDYDVLSTFVK 445
Db 546 TIRDPCTRKTFPDYDVLSTFVK 570

RESULT 10

US-09-861-696-56
Sequence 56, Application US/09861696
Patent No. US2002007053A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard P.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOALPYRUVYL-SHIKIMATE-3-PHOSPHATE SYNTHASES
FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
CURRENT APPLICATION NUMBER: US/09/861,696
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/137,440
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: US 08/833,485
PRIOR FILING DATE: 1997-04-07
PRIOR APPLICATION NUMBER: US 08/306,063
PRIOR FILING DATE: 1994-09-13
PRIOR APPLICATION NUMBER: US 07/749,611
PRIOR FILING DATE: 1991-08-28
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR FILING DATE: 1990-08-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.0
SEQ ID NO 56
LENGTH: 444
TYPE: PRT
ORGANISM: Zea mays
US-09-861-696-56

Query Match 97.3%; Score 2194.5; DB 9; Length 444;
Best Local Similarity 97.3%; Pred. No. 1.8e-193;
Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
QY 1 AGAEEVVLQPIKEISGVVVKLPGSKSLSNRILLLSALAEGLTVVDNLNLSSEVDHYMGLAK 60
Db 1 AGAEEVVLQPIKEISGVVVKLPGSKSLSNRILLLSALAEGLTVVDNLNLSSEVDHYMGLAK 60
QY 61 TLGLSEADKAAKRAVAVVCGGKFPVEKDAKEEVQLFLGNAGTAMRSLLTAATTAAGNAT 120
Db 61 TLGLSEADKAAKRAVAVVCGGKFPVE-DAKEEVQLFLGNAGTAMRSLLTAATTAAGNAT 119
QY 121 YVLGVPRMRERPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 180
Db 120 YVLGVPRMRERPIDLVVGLKQLGADVDCFLGTDCCPVRVVGIGLPGKVKLSGSIS 179
QY 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 240
Db 180 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSDRFPYIKGGQ 239
QY 241 KXSPKNAAYVEGDASSASYFLAGAAITGGTVYVEGCGTTSLOGDVYKAEVLEMMGAKVTW 300
Db 240 KXSPKNAAYVEGDASSASYFLAGAAITGGTVYVEGCGTTSLOGDVYKAEVLEMMGAKVTW 299
QY 301 TETSVTVTGPOREPFGKHLKALIDVNMNMKMPDVAMTLAVVALLFADGPTAIRDVASRWYKE 360
Db 300 TETSVTVTGPOREPFGKHLKALIDVNMNMKMPDVAMTLAVVALLFADGPTAIRDVASRWYKE 359
QY 361 TERMAVIRTELTKLGASVEEGLDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACADVPV 420

Db 360 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACAEVAV 419
QY 421 TIRDPGCTRKTPFDYFDVLTSTFVKN 445
Db 420 TIRDPGCTRKTPFDYFDVLTSTFVKN 444

RESULT 11

US-09-464-099A-56
; Sequence 56, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYHOSTE TOLERANT 5-ENOLPRUVYLSHIKIMATE-3-PHOSPHATE SYNTASES
; FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 444
; TYPE: PRN
; ORGANISM: Zea mays
US-09-464-099A-56

Query Match 97.3%; Score 2194.5; DB 9; Length 444;

Best Local Similarity 97.3%; Pred. No. 1.8e-193; Matches 433; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLALAEGLTVVDNLNSEDVHYMLGALK 60
Db 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLALAEGLTVVDNLNSEDVHYMLGALK 60
QY 61 TLGLSVADKAKRAVAVVGGCGKFPVEKDAKEVOLFGLNAGTAMRSLTAATTAAGNAT 120
Db 61 TLGLSVADKAKRAVAVVGGCGKFPVEKDAKEVOLFGLNAGTAMRSLTAATTAAGNAT 119
QY 121 YVLGVPKMRERPIGDLVGLKQLGADVDCFLGTDCPPVAVKIGGLPGKVKLSGSIS 180
Db 121 YVLGVPKMRERPIGDLVGLKQLGADVDCFLGTDCPPVAVKIGGLPGKVKLSGSIS 179
QY 181 QYLSALLMAAPLALGDVEIBIIDKLISIPYEMTLRMERFGVKAHSWSMDRFPYIKGGQ 240
Db 181 QYLSALLMAAPLALGDVEIBIIDKLISIPYEMTLRMERFGVKAHSWSMDRFPYIKGGQ 239
QY 241 KYSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
Db 241 KYSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 299
QY 301 TETSVTVTGPOREPGRKHLKALDVNNKMPDVAMTLAVVALPADGPTAIRVVASRWYKE 360
Db 301 TETSVTVTGPOREPGRKHLKALDVNNKMPDVAMTLAVVALPADGPTAIRVVASRWYKE 359
QY 361 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPY 420
Db 361 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPY 419
QY 421 TIRDPGCTRKTPFDYFDVLTSTFVKN 445

Db 420 TIRDPGCTRKTPFDYFDVLTSTFVKN 444

RESULT 12

US-10-437-963-162988
; Sequence 162988, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162988
; LENGTH: 515
; TYPE: PRN
; ORGANISM: Oryza sativa
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62025C.1.pcp
US-10-437-963-162988

Query Match 96.0%; Score 2165; DB 16; Length 515;

Best Local Similarity 95.1%; Pred. No. 1.2e-190; Matches 423; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLALAEGLTVVDNLNSEDVHYMLGALK 60
Db 71 AGAEEVVLQPIKEISGVVGLPGSKSLSNRIILLALAEGLTVVDNLNSEDVHYMLGALK 130
QY 61 TLGLSVADKAKRAVAVVGGCGKFPVEKDAKEVOLFGLNAGTAMRSLTAATTAAGNAT 120
Db 131 ALGLSVADKAKRAVAVVGGCGKFPVEKDAKEVOLFGLNAGTAMRSLTAATTAAGNAT 190
QY 121 YVLGVPKMRERPIGDLVGLKQLGADVDCFLGTDCPPVAVKIGGLPGKVKLSGSIS 180
Db 191 YVLGVPKMRERPIGDLVGLKQLGADVDCFLGTDCPPVAVKIGGLPGKVKLSGSIS 250
QY 181 QYLSALLMAAPLALGDVEIBIIDKLISIPYEMTLRMERFGVKAHSWSMDRFPYIKGGQ 240
Db 251 QYLSALLMAAPLALGDVEIBIIDKLISIPYEMTLRMERFGVKAHSWSMDRFPYIKGGQ 310
QY 241 KYSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 300
Db 311 KYSPKNAVVEGDASASVFLAGAAITGCTVVEGCGTTSLOGDVKFAVLEMMGAKVTM 370
QY 301 TETSVTVTGPOREPGRKHLKALDVNNKMPDVAMTLAVVALPADGPTAIRVVASRWYKE 360
Db 371 TETSVTVTGPOREPGRKHLKALDVNNKMPDVAMTLAVVALPADGPTAIRVVASRWYKE 430
QY 361 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPY 420
Db 431 TERMVAIKTELTKLGASVEEGPDYCIITPEKLNVTALIDTYDDHRMAMAFSLAACADVPY 490
QY 421 TIRDPGCTRKTPFDYFDVLTSTFVKN 445
Db 491 TIRDPGCTRKTPFDYFDVLTSTFVKN 515

RESULT 13

US-10-214-766-20
; Sequence 20, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg

```

; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-214-766-20

Query Match      85.5%; Score 1929; DB 14; Length 391;
Best Local Similarity 95.9%; Pred. No. 4,8e-169;
Matches 375; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 55 MLGALKTGLSVEADKAKRAVAVVCGGKFPVEKDAKEVQLFLGNAAGTAMRSITTAATAVA 114
D 1 MLRLKALGSLSEADKAKRAVAVVCGGKFPVEKDAKEVQLFLGNAAGTAMRPLTAATAVA 60
QY 115 AGGNATYVDGVPRMRERPIGDLVVGKQAGADVDFLGTDCPPVAVKIGLPGSKVKL 174
D 61 AGGNATYVDGVPRMRERPIGDLVVGKQAGADVDFLGTDCPPVAVKIGLPGSKVKL 120
QY 175 SSGISISQYLSALLMAAPLADGVEIEIIDKLISIPYEMTLRLMERGVKAHSDSDWDRF 234
D 121 SSGISISQYLSALLMAAPLADGVEIEIIDKLISIPYEMTLRLMERGVKAHSDSDWDRF 180
QY 235 YIKGGQKYSKPKNAVYEGDSSASYFLAGAAITGGTVEGCGTTSLOGDVYKFAVLEMM 294
D 181 YIKGGQKYSKPKNAVYEGDSSASYFLAGAAITGGTVEGCGTTSLOGDVYKFAVLEMM 240
QY 295 GATVYTESVTYTGPRERPRKHLKAIDVNNKMPDVAMTLAVVALPADGPTAIRDVA 354
D 241 GATVYTESVTYTGPRERPRKHLKAIDVNNKMPDVAMTLAVVALPADGPTAIRDVA 300
QY 355 SWEVKETERVVAIRTELTKGASVEEGLDYCIITPEKLNVTAIIDYDDHRMAAFSLAA 414
D 301 SWEVKETERVVAIRTELTKGASVEEGLDYCIITPEKLNVTAIIDYDDHRMAAFSLAA 360
QY 415 CADVPYTIKDPGCTRKTPFDYDVLSTFYKN 445
D 361 CADVPYTIKDPGCTRKTPFDYDVLSTFYKN 391

RESULT 14
US-09-861-696-55
; Sequence 55, Application US/09861696
; Patent No. US20020007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOUPRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55

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; LENGTH: 444
; TYPE: PRT
; ORGANISM: Petunia x hybrida
; US-09-861-696-55

Query Match      85.4%; Score 1927; DB 9; Length 444;
Best Local Similarity 84.4%; Pred. No. 8,9e-169;
Matches 372; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 5 EVVLQPIKEISGVKLPKSKLSNRIILLALAEGLTVVDNLINSDVHYMIGALKTLGL 64
D 4 EIVLQPIKEISGVKLPKSKLSNRIILLALAEGLTVVDNLINSDVHYMIGALKTLGL 63
QY 65 SVEADKAKRAVAVVCGGKFPVEKDAKEVQLFLGNAAGTAMRSITTAATAVNAAGNATYVD 124
D 64 HVEBDANORAAVVEGGGLPVGKESKEBIQLFLGNAAGTAMRPLTAATAVAGNSRYVD 123
QY 125 GVPKMERPIGDLVVGKQAGADVDFLGTDCPPVAVKIGLPGSKVKLSGISISQYLS 184
D 124 GVPKMERPIGDLVVGKQAGADVDFLGTDCPPVAVKIGLPGSKVKLSGISISQYLS 183
QY 185 ALLMAAPLADGVEIEIIDKLISIPYEMTLRLMERGVKAHSDSDWDRFYIKGGQKYS 244
D 184 ALLMAAPLADGVEIEIIDKLISIPYEMTLRLMERGVKAHSDSDWDRFYIKGGQKYS 243
QY 245 PKNAVYEGDSSASYFLAGAAITGGTVEGCGTTSLOGDVYKFAVLEMMGAKVTTERS 304
D 244 PKNAVYEGDSSASYFLAGAAITGGTVEGCGTTSLOGDVYKFAVLEMMGAKVTTERS 303
QY 305 VTYTGPRERPRKHLKAIDVNNKMPDVAMTLAVVALPADGPTAIRDVAWRVKTERR 364
D 304 VTYTGPRERPRKHLKAIDVNNKMPDVAMTLAVVALPADGPTAIRDVAWRVKTERR 363
QY 365 VAIRTELTKGASVEEGLDYCIITPEKLNVTAIIDYDDHRMAAFSLAACADVPTIRD 424
D 364 VAIRTELTKGASVEEGLDYCIITPEKLNVTAIIDYDDHRMAAFSLAACADVPTIRD 423
QY 425 PGCTRKTPFDYDVLSTFYKN 445
D 424 PGCTRKTPFDYDVLSTFYKN 444

RESULT 15
US-09-464-099A-55
; Sequence 55, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOUPRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Petunia x hybrida
; US-09-464-099A-55

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